

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 17, 2002, 01:49:05 ; Search time 1825.37 Seconds

(without alignments)
15401.427 Million cell updates/sec

Title: US-09-728-421d-6

Sequence: 1 atgcgcctaagtgtccctg.....ttgaactacagaccacgcc 966

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

T number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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19: em_mu:*
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39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	966	100.0	966	10 AF216747	AF216747 Mus muscu
2	966	100.0	2718	6 AX100591	AX100591 Sequence
3	966	100.0	2718	10 AF199027	AF199027 Mus muscu
4	966	100.0	2803	10 BC029227	BC029227 Mus muscu
5	956.8	99.0	1759	6 AX100593	AX100593 Sequence
6	956.8	99.0	1759	10 AF394451	AF394451 Mus muscu
7	360	37.3	158049	2 AC015891	AC015891 Mus muscu
8	299.6	31.0	909	9 AF216749	AF216749 Homo sapi
9	299.6	31.0	953	6 AX100595	AX100595 Sequence
10	299.6	31.0	1009	9 AF199028	AF199028 Homo sapi
11	299.6	31.0	1548	6 AX083950	AX083950 Sequence
12	299.6	31.0	1572	9 AF289028	AF289028 Homo sapi
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14	293.6	30.4	716	6 AX083952	AX083952 Sequence
15	205.2	21.2	118361	2 AC109383	AC109383 Rattus no
16	155.4	16.1	2240	9 AK090492	AK090492 Homo sapi
17	152.6	15.8	2706	9 IROBST054	AL355690 Homo sapi
18	145.2	15.0	36230	9 AP001059	AP001059 Homo sapi
19	145.2	15.0	39553	9 AP001058	AP001058 Homo sapi
20	145.2	15.0	340000	9 AP001753	AP001753 Homo sapi
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22	44.4	4.6	125020	9 AF429315	AF429315 Homo sapi
23	41.1	4.2	290080	2 AC096333	AC096333 Rattus no
24	40.2	4.2	125020	9 AF429315	AF429315 Homo sapi
25	40.2	4.2	205509	10 AL731853	AL731853 Mouse DNA
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37	38.8	4.0	261224	10 AL645527	AL645527 Mouse DNA
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39	38.6	4.0	174571	2 AC106476	AC106476 Rattus no
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44	38.2	4.0	97902	9 AL596118	AL596118 Human DNA
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ALIGNMENTS

RESULT 1	AF216747	966 bp	musculus	linear	23-MAR-2000
LOCUS	AF216747				
DEFINITION	Mus musculus B7-related protein 1 mRNA, partial cds.				
ACCESSION	AF216747				
VERSION	AF216747.1	GI:7288510			
KEYWORDS					
SOURCE					
ORGANISM					
	Mus musculus.				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
REFERENCE	1 (bases 1 to 966)				
AUTHORS	Yoshinaga,S.K., Whoriskey,J.S., Khare,S.D., Sarmiento,U., Guo,J.,				
	Horan,T., Shih,G., Zhang,M., Cocchia,M.A., Kohno,T.,				
	Tafuri-Biadt,A., Campbell,P., Chang,D., Chiu,L., Dai,T., Duncan,G.,				

LOCUS	AF199027	2718 bp	mRNA	linear	ROD 17-FEB-2000
DEFINITION	Mus musculus B7-1-like protein (G150) mRNA, complete cds.				
ACCESSION	AF199027				
VERSION	AF199027.1	GI:6983941			
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Db	187	CTCTGTCGCTCTGACAGACTGAAAGTGGGTGCAATGGTGGGAGCAATGTGGTCTC	246		
Oy	181	ACCTGATTGACCCCCACAGAGCCATTTTCAACTTGAGTGTCTGTATGTTGGCAA	240		
Db	247	ACCTGATTGACCCCCACAGAGCCATTTTCAACTTGAGTGTCTGTATGTTGGCAA	306		
Oy	241	ATCGAAACCCAGAAAGTTTCGGGACTTACTACCTGCTTCAAGCTCCAGGATCAT	300		
Db	307	ATCGAAACCCAGAAAGTTTCGGGACTTACTACCTGCTTCAAGCTCCAGGATCAT	366		
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Db	367	GTGAGCAGTTCTTACAAAGAACAGGGGCCATCTGTCCCTGGACTCCATGAAGCAGGTAAC	426		
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Db	427	TTTCTCTCTTACCTGAAGAATGTCAACCCCTCAGAGATACCCAGAGTTCAACATGCCGGTA	486		
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Oy	481	GCAGCAAACTTCAGTACACACTCTCATCAGACACTCTGTATAGTCCAAACCCGGCCAGAA	540		
Db	547	GCAGCAAACTTCAGTACACACTCTCATCAGACACTCTGTATAGTCCAAACCCGGCCAGAA	606		
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Db	1027	CACGCC 1032			

SOURCE	Mus musculus.
ORGANISM	Mus musculus.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2718)
AUTHORS	Ling,V., Wu,P.W., Finnerly,H.F., Bean,K.M., Spaulding,V., Fouser,L.A., Leonard,J.P., Hunter,S.E., Zollner,R., Thomas,J.L., Miyashiro,J.S., Jacobs,K.A. and Collins,M. Cutting edge: identification of GL50, a novel B7-1-like protein that functionally binds to ICOS receptor J. Immunol. 164 (4), 1653-1657 (2000)
TITLE	
JOURNAL	
MEDLINE	20126021
PUBMED	10657606
REFERENCE	2 (bases 1 to 2718)
AUTHORS	Ling,V.
TITLE	Direct Submission
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Dd	367 GTGACAGTTTCTCAAGAACAGGGGCATCTGTCCCTGAGACTCCATGAAGCAGGATAAC 426
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QY 961 CACGCC 966
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RESULT 4
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DEFINITION Mus musculus, lcos ligand, clone MGC:35971 IMAGE:4217333, mRNA,
complete cds.
VERSION BC029227.1 GI:22137738
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu

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Matches 966; Conservative 0; Mismatches 0;

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SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1759)
AUTHORS Ling, V., Wu, P.W., Miyashiro, J.S., Marusic, S., Finnerty, H.F. and Collins, M.
TITLE Differential expression of inducible costimulator-1 ligand variants: lymphoid regulation of mouse GL50-B and human GL50 molecules
JOURNAL J. Immunol. 166 (12), 7300-7308 (2001)
MEDLINE 21286479
PUBMED 11390480
REFERENCE 2 (bases 1 to 1759)
AUTHORS Ling, V., Wu, P.W., Miyashiro, J., Marusic, S., Finnerty, H.F. and Collins, M.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-2001) Immunology, Genetics Institute/Wyeth Ayerst, 200 Cambridge Park Drive, Cambridge, MA 02140, USA
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QY 721 CTGTGCTGCGTAGAAGATGTGCTCTCCACGAAACATCATAGCATTAAGCCAGGACAA 780
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QY 841 CTGTGCCCGCTCTGCTGCTACTGTGCGGACGGCATTCGTTCCCTCATATATACAGA 900
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Db 901 GCGACGCTGCCACCGAAGATATACAGACCCAAAGACTGTACAGTTGAATTACAGAC 960
RESULT 7
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LOCUS Mus musculus chromosome 10 clone RP21-522L13 map 10, *** SEQUENCING
DEFINITION
IN PROGRESS ***, 6 unordered pieces.
ACCESSION AC015891
VERSION AC015891.14 GI:10945782
KEYWORDS HTG, HTGS, PHASE1, HTGS_FULLTOP, HTGS_ACTIVEFIN.
SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 158049)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Mus musculus chromosome 10, clone RP21-522L13
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 158049)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckery, R., Boguslavsky, L., Boukhalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collumore, A., Cooke, P., DeRellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczy, J., Lien, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McEwan, A., McKernan, K., McDonald, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange, J., Stojanovic, N., Sudmanian, A., Talamas, J., Testa, S., Tjelle, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome

Db 254 TGATGTCAACGGCCGGCATGCTGGGGGGGAGACTTCTCCCTGGCTTTGTTCAACGTCACCC 313
Qy 389 CTCAGGATACCAGAGTTTCACATGCCGGGATATTTATGAAATACGCCACAGAGTTAGTCA 448
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Qy 809 CACAGAAACCCACAATA 826
Db 728 CAGAGATCCAGTCAAGTA 745

RESULT 9
LOCUS AX100595 953 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 5 from Patent WO0121796.
ACCESSION AX100595
VERSION AX100595.1 GI:13619598
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 953)
AUTHORS Ling, V., and Dunnussli-Joannopolulos, K.
TITLE G150 molecules and uses therefor
PATENT: WO 0121796-A 5 29-MAR-2001;
JOURNAL GENETICS INSTITUTE, INC. (US)
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BASE COUNT 210 a 277 c 276 g 190 t

Query Match 31.0%; Score 299.6; DB 6; Length 953;
Best Local Similarity 64.8%; Pred. No. 9e-82;
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Qy 89 GTCCTGCTGTCTTCTGCTGTGAGACGCTGTGCTCTGACAGACTGAG 148
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Qy 209 TCACTTGAGTGTGTATGTCTATTGGCAAAATGCAAAACCCCAAACTTCGGGACTT 268
Db 157 TTGATTTAAATGATTTTACGTATTTGCAAAACCAAGTGAAGTGAACCGTGGTGA 216
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Qy 809 CACAGGAAACCCACAATA 826
Db 751 CAGAGATCCAGTCAAGTA 768

RESULT 10
LOCUS AF199028 1009 bp mRNA linear PRI 17-FEB-2000
DEFINITION Homo sapiens B7-like protein (G150) mRNA, complete cds.
ACCESSION AF199028
VERSION AF199028.1 GI:6983943
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1009)
AUTHORS Ling, V., Wu, P.-W., Finerly, H.F., Bean, K.M., Spaulding, V.,
Fouser, L.A., Leonard, J.P., Hunter, S.E., Zollner, R., Thomas, J.L.,
Miyashiro, J.S., Jacobs, K.A., and Collins, M.
TITLE Cutting edge: identification of G150, a novel B7-like protein that
functionally binds to ICOS receptor
JOURNAL J. Immunol. 164 (4), 1653-1657 (2000)
MEDLINE 20126021
PUBMED 10657606


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Db 608 TGAGATGTCGACGAGACCCCGACGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
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Db 668 ACCAGAACATCACTAGCATTAAGCCAGGAGAAAGTTTCACTGGAATAACACAAAGATCA 727
QY 809 CACAGAAACCCACATA 826
Db 728 CAGAGAAATCAGTCACTA 745

RESULT 12
DEFINITION Homo sapiens transmembrane protein B7-H2 ICOS ligand mRNA, complete cds.
ACCESSION AF289028
VERSION AF289028.1 GI:9858866
KEYWORDS Homo sapiens.
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1572)
AUTHORS Wang, S., Zhu, G., Chapoval, A.I., Dong, H., Tamada, K., Ni, J. and Cheng, L.
TITLE Costimulation of T cells by B7-H2, a B7-like molecule that binds ICOS
JOURNAL Blood 96 (8), 2808-2813 (2000)
MEDLINE 20477846
PUBMED 11023515
REFERENCE 2 (bases 1 to 1572)
AUTHORS Wang, S., Zhu, G., Ni, J. and Chen, L.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-2000) Immunology, Mayo Clinic, 200 First Street SW, Rochester, MN 55905, USA
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BASE COUNT 325 a 480 c 471 g 296 t
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Query Match 31.0%; Score 299.6; DB 9; Length 1572;
Best Local Similarity 64.8%; Pred. No. 9,5e-82;
Matches 478; Conservative 0; Mismatches 254; Indels 6; Gaps 2;

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QY 209 TCAACTGAGTGCTGTATGTTATTTGGCAATCGAAAACCCAGAGTTTGCTGACTT 268
Db 258 TTGATTTAATATATGTTATGTTATTTGGCAATCGAAAACCCAGAGTTTGCTGACTT 317
QY 269 ACTACCTGCTTACAAAGTCTCCAGGATCAATGTGACAGTTCTTCAACAAGACGGGCC 328
Db 318 ACCACATCCCAAGAAACAGCTCTTGGAAACGTGGACAGCCGCTACCGAACCAGGCC 377
QY 329 ATCTGTCCCTGACATCAGTAAGACGGGTAACTTCTCTGTATACCTGAAGAAATGTCACC 388
Db 378 TGATGTACACCGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 437
QY 389 CTCAGATACCCAGAGTTCACATGCGCGGTATTATGAAATACAGCAGAGATTAGTCA 448
Db 438 CCCAGACAGCAGAAAGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494
QY 449 AGATCTTGAAGAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 508
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QY 509 GCACCTCTATAGCTTCAACCCGGCCAGAACGTATCAACCTGCAATGTCAGAAATG 568
Db 555 GGGCCCCCAGACGCCCTCCAGG---ATGACCTCACTTCACTGCTGCTGCTGCTGCTGCT 611
QY 569 GCTACCCAGAGCCCAACCTGTATTGATCAACAGCAGACATAGCTAATAGACAGG 628
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QY 629 CTCCTGAGAAATACACTGCTACTGTGAGCAAGTTGGCGCTGATGATGTAATACGACAT 688
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QY 689 TAAGCTCCCTGTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 748
Db 732 TGAGATGTCGACGAGACCCCGACGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
QY 749 ACCAGAACATCACTAGCATTAAGCCAGGAGAAAGTTTCACTGGAATAACACAAAGACCC 808
Db 792 ACCAGAACATCACTAGCATTAAGCCAGGAGAAAGTTTCACTGGAATAACACAAAGATCA 851
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Db 852 CAGAGAAATCAGTCACTA 869

RESULT 13
LOCUS AB014553 4358 bp mRNA linear PRI 06-FEB-1999
DEFINITION Homo sapiens mRNA for KIAA0653 protein, partial cds.
ACCESSION AB014553
VERSION AB014553.1 GI:3327119
KEYWORDS Homo sapiens adult male brain cDNA to mRNA, clone.lib.pb1uescriptII
SOURCE SK plus clone:HK01718.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Ishikawa, K., Nagase, T., Suyama, M., Miyajima, N., Tanaka, A., Kotani, H., Nomura, N. and Ohara, O.
TITLE Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro
JOURNAL DNA Res. 5 (3), 169-176 (1998)
MEDLINE 98403880
REFERENCE 2 (bases 1 to 4358)
AUTHORS Ohara, O., Suyama, M., Nagase, T. and Ishikawa, K.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1998) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)

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Source

[illegible]

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Best Local Similarity	64.88;	Pred. No. 1e-81;		
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Db	796	AGCAAGAACTGTACTGTGGCAGCCAGACAGGAAATGACATCCGAGAGAGACAAAGATCA	855
QY	809	CACAGGAAACCCCAATA	826
Db	856	CAGAGAAATCCAGTCA	873

RESULT 14
AX083952

SEQUENCE	716 bp	DNA	
DEFINITION	Sequence 3 from Patent WO0112658.	linear	PAT 28-FEB-2001
ACCESSION	AX083952		

AX083952.1 GI:13185509

SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutollostomi;

REFERENCE
1 (bases 1 to 716)
Mammalia; Eucnecida; Primates; Catarrhini; Homnidae; Homo.

TITLE Human Icos Heard and collected

JOURNAL
Patent: WO 0112658-A 3 22-FEB-2001,
ISTS INVENTION

Location/Qualifiers

/organism="Homo sapiens"

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BASE COUNT      164 a      206 c      201 g      145 t
ORIGIN          /organism="Homo sapiens"
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□

Query Match	30.4%	Score 293.6;	DB 6;	Length 716;
Best Local Similarity	65.4%;	Pred. No. 6.5e-80;		
Matches 463;	Conservative 0;	Mismatches 239;	Indels 6;	Gaps 2

QY	89	GGCTTGGGCTGTGCTTCCCTCCTGTGAGCAGCCCTGTGTCTGCTCTTGACAGAGACTGAAG	14
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QY	149	TGCGTGCAATGGTGGGAGCAATGATGTGCTCAGCTGATGATTGACCCCAAGAGCCATT	20
Db	74	TCAGAGCAGATGGTAGGAGCAGAGCTGAGACTAGCTGGCGCTTGAGGAGAAAGCCGTT	13
QY	209	TCAACTTGAGGGGTCTGTATGTCTATTGGCAATCGAAAACCCAGAAATTTCGGTACTT	26
Db	134	TTGATTTTAATGATGTTTACGTAATATGGCAACAGAGATCGAAAACCGTGTAAGCT	19
QY	269	ACTACCTGCCTTACAAGTCTCCAGGGATCAATGAGAGATGCTCTACAAAGACAGGGGCC	32
Db	194	ACGCACATCCCAAGAACAGCTCTTTGAAAAACGTGACAGCCGCTACCGGAACCGAGGCC	25
QY	329	ATTCGTCCCTGGAGCTGCATGAGACGAGGTAACCTTCTCTGTACTGAAGAAATGTACCC	38
Db	254	TGATGTACCGCGGCAATGCTGCGGGGCGACTTCTCCCTGCGCTTTTCACAGTCAACC	31
QY	389	CTCAGATACCCAGAGTTCATCATCCGCGGATATTGATTAAGCCACAGAGTTAGTCA	44
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QY	509	GCACCTTATATAGTCTCAACCGGGGCGAGGAAGTACCTACACCTGCTATGTCCAAAGT	56
Db	431	GGCGCCCCACAGAGCCCTTCCAGG--ATAGATCTCACTTTCACGTTGATCTCACTTAACG	48

REFERENCE	2 (bases 1 to 118361)
AUTHORS	Worley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (04-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 118361)
AUTHORS	Worley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (13-Jul-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Jul 12, 2002 this sequence version replaced gi:18846801.
	----- Genome Center -----
	Center: Baylor College of Medicine
	Center code: BCM
	Web site: http://www.hgsc.bcm.tmc.edu/
	Contact: hgsc-help@bcm.tmc.edu
	----- Project Information -----
	Center project name: GPMN
	Center clone name: CH230-48B22
	----- Summary Statistics -----
	Sequencing vector: Plasmid
	Chemistry: Dye-terminator Big Dye: 100% of reads
	Assembly program: Phrap; version 0.990329
	Consensus quality: 68562 bases at least Q40
	Consensus quality: 72926 bases at least Q30
	Consensus quality: 77045 bases at least Q20

	* NOTE: Estimated insert size may differ from sequence length
	* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html)
	* NOTE: This is a 'working draft' sequence. It currently
	* consists of 63 contigs. The true order of the pieces
	* is not known and their order in this sequence record is
	* arbitrary. Gaps between the contigs are represented as
	* runs of N, but the exact sizes of the gaps are unknown.
	* This record will be updated with the finished sequence
	* as soon as it is available and the accession number will
	* be preserved.
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*	2926: 2925: gap of unknown length
*	3926: 3973: contig of 1048 bp in length
*	4074: 4073: gap of unknown length
*	5638: 5637: contig of 1564 bp in length
*	5738: 5737: gap of unknown length
*	7020: 7020: contig of 1283 bp in length
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*	14405: 14504: gap of unknown length
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*	15702: 15802: gap of unknown length
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*	17011: 17110: gap of unknown length
*	17111: 18152: contig of 1042 bp in length
*	18153: 18252: gap of unknown length
*	18253: 19761: contig of 1509 bp in length
*	19762: 19861: gap of unknown length
*	19862: 21045: contig of 1184 bp in length
*	21046: 21145: gap of unknown length
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QY 481 GCAGCAAACTTCGTGTCACCTGTCATCAGCACCCTCTGATAGCTCCAAACCCGGGCCAGGAA	540			
Db 52095 GCAGCAAACTTCGTGTCACCTGTCATCAGCACCCTCTGAGGAGCTTCAGCCCTGGCCAGGAA	52154			
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Db 52155 CGCACCCTCATTGGATGTCGCAAGATGGCTACCCAGAGCCCAACCTGTATTGGATCAAC	52214			
QY 601 ACAAGGGCAATAGCCTTAATAGACAAGGCTCTGCAGAAATACACTGTCTACTTGAACAAG	660			
Db 52215 AAGAGGGCAATAGCCTTAATAGACAAGGCTCTGCAGAAATACACTGTCTACTTGAACAAG	52274			
QY 661 TTGGGCGCTGATGATGTATATGAGCAATTAAGGCTCCCTTGGACATCTCGTGGGATGTT	720			
Db 52275 TTGGGCGCTGATGATGTATATGAGCAATTAAGGATCCCTTGGACCCCATGTGGGATG-T	52333			
QY 721 CTGTGCTCGTAGAGAAATGTGGCTTCCAC 750				
Db 52334 ATCTGCTGTAGAGAAATGTGGCTTCCAC 52363				

Search completed: November 17, 2002, 04:44:04
 Job time : 1953.37 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 17, 2002, 01:43:50 ; Search time 180.003 Seconds

(without alignments)
12085.504 Million cell updates/sec

Title: US-09-728-421D-6

Perfect score: 966
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 112599159 residues

T number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT: *
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9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT: *
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16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT: *
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT: *
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT: *
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT: *
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT: *
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT: *
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: *
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	966	100.0	966	21	AAA64555
2	966	100.0	966	24	ABK87592
3	966	100.0	2718	22	AAAF7919
4	956.8	99.0	1759	22	AAAF7920
5	691.4	71.6	1830	22	AAAF7942
6	538.2	55.7	2729	24	ABL35026
7	450.6	46.6	545	21	AAA43831
8	299.6	31.0	864	21	AAA64556
9	299.6	31.0	864	24	ABK87593

10	299.6	31.0	906	22	AAH7869	Nucleotide sequenc
11	299.6	31.0	953	21	AAAF79921	Nucleotide sequenc
12	299.6	31.0	1294	22	AAA64557	DNA sequence encod
13	299.6	31.0	1294	24	ABK87594	CDNA encoding huma
14	299.6	31.0	1453	24	AAH7870	Nucleotide sequenc
15	299.6	31.0	1548	22	AA500423	Human B7-3 CDNA.
16	299.2	31.0	2114	22	ABA06726	Human CDNA seq ID
17	299.2	31.0	2114	22	AA528855	Human immunoglobul
18	299.2	31.0	2751	22	AAAF91911	Human secreted pro
19	298	30.8	2616	22	ABA06544	Human CDNA seq ID
20	298	30.8	2622	22	ABA06724	Human CDNA seq ID
21	298	30.8	2622	22	AA528853	Human immunoglobul
22	298	30.8	2751	22	AA528793	Human immunoglobul
23	293.6	30.4	716	22	AA500424	Human B7-3 soluble
24	273.6	28.3	1831	22	AAAF79411	Nucleotide sequenc
25	100.6	10.4	460	22	AAAF79938	CDNA clone with sl
26	37	3.8	849	20	AAZ16638	Human gene express
27	36.2	3.7	2943	8	AAH70159	Sequence encoding
28	36.2	3.7	2943	8	AAH70160	Sequence encoding
29	35.8	3.7	585	18	AAAT90022	DNA encoding heavy
30	35.4	3.7	1443	24	ABK24012	DNA encoding B7-re
31	35	3.6	37337	23	AA559518	Proiontactcerium
32	34.4	3.6	436	23	ABV34140	Human prostate exp
33	34.4	3.6	436	23	ABV43002	Human prostate exp
34	34.4	3.6	2170	23	ABL19933	Drosophila melanog
35	34.4	3.6	2294	24	ABL29367	Drosophila melanog
36	34.4	3.6	40267	24	AA518958	Human cadherin-11k
37	34.2	3.5	383	22	ABA44985	Human breast cell
38	34.2	3.5	383	22	ABA55460	Human foetal liver
39	34.2	3.5	383	22	ABA25177	Probe #3643 for ge
40	34.2	3.5	383	22	AAK03699	Human brain expres
41	34.2	3.5	383	22	AAK29160	Human bone marrow
42	34.2	3.5	383	22	AAH24065	Probe #3621 used t
43	34.2	3.5	4590	22	AAH24065	Yeast AOD9604-asso
44	34.2	3.5	7035	22	AA546689	Tumour suppressor
45	34.2	3.5	7654	22	ABA20642	Human nervous syst

ALIGNMENTS

RESULT 1	
ID	AAA64555 standard: DNA; 966 BP.
AAA64555	
AC	AAA64555:
XX	
DT	02-JAN-2001 (first entry)
XX	
DE	DNA sequence encoding a murine B7RP1 polypeptide.
XX	
KW	CRP1: CD28 related protein-1; B7RP1: B7 related protein-1;
KW	T-lymphocyte activation; type I transmembrane protein; T cell activation;
KW	T cell proliferation; T-cell mediated disorder; ss.
OS	Mus sp.
XX	
PH	key
FT	1..966
FT	Location/Qualifiers
FT	1..966
FT	/tag= a
FT	/product= "B7RP1"
FT	/note= "no termination codon given"
FT	1..138
FT	/tag= b
FT	139..966
FT	/tag= c
FT	mat_peptide
FT	
PN	WO200046240-A2.
XX	
PD	10-AUG-2000.
XX	
PF	27-JAN-2000; 2000WO-US01871.
XX	

PR 03-FEB-1999; 99US-0244448.
PR 08-MAR-1999; 99US-0264527.
XX
XX (AMGE-) AMGEN INC.
XX Yoshinaga SK:
PI WPI: 2000-543476/49.
XX P-PSDB: AAB08725.
DR
XX Novel nucleic acids encoding the proteins CRP-1 and B7Rpl are useful
PR in the treatment, prevention and diagnosis of T cell mediated disorders
PT
XX
XX
PS Claim 2: Fig 2A; 174pp; English.
PS
XX The present sequence encodes a B7Rpl (B7 related protein-1)
CC polypeptide. The specification also describes a CRP1 (CD28 related
CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
activation, and represent a receptor-ligand pair. CRP1 and B7Rpl are
predicted to be a type I transmembrane protein. The nucleic acids are
useful for regulating T cell activation or proliferation in an animal.
CC The polypeptides are useful for treating, preventing ameliorating or
diagnosing a T-cell mediated disorder in an animal. They can also be
used to identify test molecules that bind to the polypeptides.
CC
XX
SQ Sequence 966 BP; 247 A; 256 C; 229 G; 234 T; 0 other;

Query Match 100.0%; Score 966; DB 21; Length 966;
Best Local Similarity 100.0%; Pred. No. 7.2e-298;
Matches 966; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGAGCTAAAGTCCCTTTGTCCTGGGACGAGCAGCCTTTGGAGAAG 60
DB 1 ATGCGAGCTAAAGTCCCTTTGTCCTGGGACGAGCAGCCTTTGGAGAAG 60
QY 61 CTCGATGTTCTAGCGGGTCTTTCTGCTGGTCTCTTCTGCTGTTGAGCAGC 120
DB 61 CTCGATGTTCTAGCGGGTCTTTCTGCTGGTCTCTTCTGCTGTTGAGCAGC 120
QY 121 CTCGTGCTGCTCTGTCAGAGACTGAATGCGTGCATATGTTGGGCAATGTCGCTC 180
DB 121 CTCGTGCTGCTCTGTCAGAGACTGAATGCGTGCATATGTTGGGCAATGTCGCTC 180
QY 181 AGCTGATGAGCCGCCACAGAGCCATTTCACTGAGTGGCTGATCTTATTTGGCAA 240
DB 181 AGCTGATGAGCCGCCACAGAGCCATTTCACTGAGTGGCTGATCTTATTTGGCAA 240
QY 241 ATCGAAAACCCAGAGTTCGCTGACTTACTACTGCTCTTACAGTCTCCAGGATCAAT 300
DB 241 ATCGAAAACCCAGAGTTCGCTGACTTACTACTGCTCTTACAGTCTCCAGGATCAAT 300
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DB 301 GTGGAGAGTTCCTACAGAAAGAGGGGCCATGTCCTGAGCTCCATGAAGCGGGTAAAC 360
QY 361 TTCTCTCTGACTGGAAGATGTCACCCCTCAGAGATACCAGAGTTCACATCCCGGTA 420
DB 361 TTCTCTCTGACTGGAAGATGTCACCCCTCAGAGATACCAGAGTTCACATCCCGGTA 420
QY 421 TTTATTAATACAGCCACAGAGTGTAGTCAAGATCTTGAAGAGGTGGTCCGCTGTG 480
DB 421 TTTATTAATACAGCCACAGAGTGTAGTCAAGATCTTGAAGAGGTGGTCCGCTGTG 480
QY 481 GCAGAACTTCGACCTGTCATCAGACACTGTGATAGTCCAAACCGGGCCAGGAA 540
DB 481 GCAGAACTTCGACCTGTCATCAGACACTGTGATAGTCCAAACCGGGCCAGGAA 540
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DB 541 CGTACCTACACCTGATGTCAGAAATGCTACCCAGAGCCCAACCTGATTTGGATCAAC 600
QY 601 ACAGAGGACATATGCTTAATAGACAGGCTCTGACAGATTAACCTGCTACTTGAACAG 660

DB 601 ACAAGGACATATAGCCTATATAGACAGGCTCTGACAGATTAACACTGTACTTGAACAG 660
QY 661 TTGGGCTGTATGATGTAATACGACATTAAGCTCCCTTGGACATCTCGTGGGATGTT 720
DB 661 TTGGGCTGTATGATGTAATACGACATTAAGCTCCCTTGGACATCTCGTGGGATGTT 720
QY 721 CTGTGCTGCTAGAGATGTGGCTCTCCACAGAACATCATTAGATGAGCCAGAGAA 780
DB 721 CTGTGCTGCTAGAGATGTGGCTCTCCACAGAACATCATTAGATGAGCCAGAGAA 780
QY 781 AGTTTCACTGAAATTAACAAAGAACCCACAGAAACCCACATATATAGTTAAAGTC 840
DB 781 AGTTTCACTGAAATTAACAAAGAACCCACAGAAACCCACATATATAGTTAAAGTC 840
QY 841 CTTGTCCCGCTCTGCTGTACTGGCGGACAGGGGATTCCTTCATCATATATACAGA 900
DB 841 CTTGTCCCGCTCTGCTGTACTGGCGGACAGGGGATTCCTTCATCATATATACAGA 900
QY 901 CGCAGCGCTCCCGACGAAAGCTATACAGAGCCACAGACTGTACACTTGAATTAACAGC 960
DB 901 CGCAGCGCTCCCGACGAAAGCTATACAGAGCCACAGACTGTACACTTGAATTAACAGC 960
QY 961 CACGCC 966
DB 961 CACGCC 966

RESULT 2
ABK87592
ID ABK87592 standard; cDNA; 966 BP.
XX
XX ABK87592;
XX
XX 07-OCT-2002 (first entry)

DE cDNA encoding murine B7 related protein-1 (B7Rpl).
XX
XX CD28 related protein-1; CRP1; T-lymphocyte costimulatory protein;
KW B7 related protein-1; B7Rpl; T-cell mediated disorder; hypersensitivity;
KW IgE-mediated disorder; allergy; sinus inflammation; immune disease;
KW graft survival; immune activation; asthma; cancer gene immunotherapy;
KW adenocarcinoma; prostate tumour; lung carcinoma; colon carcinoma; tumour;
KW T-cell dependent B-cell mediated disease; leukemia; sarcoma; melanoma;
KW viral infection; Hepatitis A virus; autoimmune disorder; psoriasis;
KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
KW diabetes; immunethrombocytopenic purpura; toxic shock syndrome;
KW bone marrow; organ transplantation; inflammatory bowel disease;
KW allsensitisation; blood transfusion; graft vs. host disease; mouse;
KW gene; ss.
XX
XX Mus musculus.
OS
XX
XX Key Location/Qualifiers
FH 1, 966
FT CDS
FT
FT /tag= a
FT /product= "B7Rpl"
FT /note= "B7 related protein-1"
FT /partial
FT /note= "No stop codon given"
PN
XX
XX WO200244364-A2.
XX
XX 06-JUN-2002.
XX
XX 28-NOV-2001; 2001WO-US44859.
XX
XX 28-NOV-2000; 2000US-0728420.
XX
XX (AMGE-) AMGEN INC.
XX (AMGE-) AMGEN CANADA INC.
XX
XX Yoshinaga SK, Mak TW, Shahinian A, Blatt AT, Senaldi G;

XX WPI: 2002-547698/58.
 XX Novel isolated T-lymphocyte costimulatory polypeptide, such as CD28
 PT related protein-1 or B7 related protein-1, useful for treating,
 PT preventing or ameliorating a T-cell mediated disorder in an animal -
 XX
 PS Claim 2; Fig 2a; 197pp; English.
 XX
 CC The invention describes an isolated T-lymphocyte costimulatory
 CC polypeptide (I), such as CD28 related protein-1 (CRP1) or B7 related
 CC protein-1 (B7RP1), and orthologues, allelic variants or alternatively
 CC sliced variants of these sequences. (I) is useful for treating,
 CC preventing, ameliorating or diagnosing a T-cell mediated disorder or a
 CC susceptibility to a T-cell mediated disorder in an animal. (I) is useful
 CC for identifying a test molecule which binds to (I) by contacting (I) with
 CC a test molecule, and determining the extent of binding of (I) to the test
 CC molecule. The method further comprises determining the activity of (I)
 CC when bound to the compound. An anti-(I) antibody is useful for
 CC suppressing an immune response in an animal, for decreasing IgE
 CC production in an animal or for treating an IgE-mediated disorder such as
 CC asthma, allergies, hypersensitivity and sinus inflammation. (I) and
 CC anti-(I) antibodies are useful for treating immune disease, graft
 CC survival, immune activation, T-cell dependent B-cell mediated disease,
 CC cancer gene immunotherapy (for e.g. leukemias, sarcomas, melanomas,
 CC adenocarcinomas, prostate tumours, lung carcinomas, colon carcinomas and
 CC other tumours), viral infection (e.g. by Hepatitis A virus), autoimmune
 CC disorders (such as rheumatoid arthritis, psoriasis, multiple sclerosis,
 CC diabetes, systemic lupus erythematosus and immunethrombocytopenic
 CC purpura), toxic shock syndrome, bone marrow and organ transplantation,
 CC inflammatory bowel disease, allersensitisation due to blood transfusions,
 CC and the treatment of graft vs. host disease, and for regulating the
 CC interaction of B7RP1 or CRP1. This sequence encodes the murine B7
 CC related protein-1 (B7RP1) a novel protein of the T-cell costimulatory
 CC pathway.
 CC
 XX
 SQ Sequence 966 BP: 247 A; 256 C; 229 G; 234 T; 0 other;
 Query Match 100.0%; Score 966; DB 24; Length 966;
 Best Local Similarity 100.0%; Pred. No. 7, 2e-298;
 Matches 966; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCAGTAAGTGTCCCTGTTTGTCTTGGGAACGAGCGCTGTTGGAAGAAG 60
 DB 1 ATGCAGTAAGTGTCCCTGTTTGTCTTGGGAACGAGCGCTGTTGGAAGAAG 60
 QY 61 CTCGATGTTCTAGCGGGTCTTTCTGCTGTGCTGTTGCTGTTGAGCAGC 120
 DB 61 CTCGATGTTCTAGCGGGTCTTTCTGCTGTGCTGTTGCTGTTGAGCAGC 120
 QY 121 CTCGTGCTGCTCTGAGAGACTGAAGTGGTGCAGCAATGTGGCTC 180
 DB 121 CTCGTGCTGCTCTGAGAGACTGAAGTGGTGCAGCAATGTGGCTC 180
 QY 181 AGCTGATTTGACCCCAAGAGCCATTTCACTGATGATGCTATTTGGCAA 240
 DB 181 AGCTGATTTGACCCCAAGAGCCATTTCACTGATGATGCTATTTGGCAA 240
 QY 241 ATGGAAGCCAGAGATTTGCTGACTACTACCTGCTTCAAGTCTCCAGGATCAAT 300
 DB 241 ATGGAAGCCAGAGATTTGCTGACTACTACCTGCTTCAAGTCTCCAGGATCAAT 300
 QY 301 GTGGAGATTCTCAAGAAAGAGGGGCAATGCTCCCTGAGCTCCATGAAGCAGGTAAC 360
 DB 301 GTGGAGATTCTCAAGAAAGAGGGGCAATGCTCCCTGAGCTCCATGAAGCAGGTAAC 360
 QY 361 TTCTCTCTGACTGAAGATGTCAACCTCAAGATACCCAGAGATTCACATGCCGGTA 420
 DB 361 TTCTCTCTGACTGAAGATGTCAACCTCAAGATACCCAGAGATTCACATGCCGGTA 420
 QY 421 TTTATATATACAGCCACAGAGTTAGTCAAGATCTTGAAGAGGTGCTGAGGCTGCTG 480
 DB 421 TTTATGAAATACAGCCACAGAGTTAGTCAAGATCTTGAAGAGGTGCTGAGGCTGCTG 480

QY 481 GCAGCAACTTACAGTACACCTGTATCAGACCTGTGATGCTCAACCCGGGCGAGAA 540
 DB 481 GCAGCAACTTACAGTACACCTGTATCAGACCTGTGATGCTCAACCCGGGCGAGAA 540
 QY 541 CGTACCTACACCTGTATGCTCAAGAAATGGCTACCCAGAGCCCAACCTGTATGATCAAC 600
 DB 541 CGTACCTACACCTGTATGCTCAAGAAATGGCTACCCAGAGCCCAACCTGTATGATCAAC 600
 QY 601 ACAAGGACATAGCTTAATAGACAGGCTCTGACAGATTAACCTGTACTTGAACAAG 660
 DB 601 ACAAGGACATAGCTTAATAGACAGGCTCTGACAGATTAACCTGTACTTGAACAAG 660
 QY 661 TTGGGCTGTATGATGATTAATACACATTAAGGCTCCCTTGACATCTGTGGGATGTT 720
 DB 661 TTGGGCTGTATGATGATTAATACACATTAAGGCTCCCTTGACATCTGTGGGATGTT 720
 QY 721 CTGTGCTGCTAGAGAAATGTGCTTCCACACAGACATCACTAGATTAGCCAGCAGAA 780
 DB 721 CTGTGCTGCTAGAGAAATGTGCTTCCACACAGACATCACTAGATTAGCCAGCAGAA 780
 QY 781 AGTTGACTGGAATATACAAAGAACCCACAGAAACCCACAAATATAGTTAAAGTC 840
 DB 781 AGTTGACTGGAATATACAAAGAACCCACAGAAACCCACAAATATAGTTAAAGTC 840
 QY 841 CTGTGCCGCTCTTCTGCTGACTGCGGAGCGGCAATGCTTCTTCATCATATACAGA 900
 DB 841 CTGTGCCGCTCTTCTGCTGACTGCGGAGCGGCAATGCTTCTTCATCATATACAGA 900
 QY 901 CGACAGCTGCCCGACGGAAGCTATACAGACCCAGAGCTGTACAGCTTACCTTACAGAC 960
 DB 901 CGACAGCTGCCCGACGGAAGCTATACAGACCCAGAGCTGTACAGCTTACCTTACAGAC 960
 QY 961 CACGCC 966
 DB 961 CACGCC 966
 RESULT 3
 AAF79919
 ID AAF79919 standard; DNA; 2718 BP.
 AC AAF79919;
 DT 11-JUN-2001 (first entry)
 XX
 DE Nucleotide sequence of a murine GL50-1.
 KW GL50: antigen; antigen presenting cell; T cell proliferation; tumour;
 KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
 KW acquired immune deficiency syndrome; AIDS; vaccine; ss.
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 67..1035
 FT /*tag= a
 FT /*product= "GL50"
 FT sig_peptide 67..195
 FT /*tag= b
 XX
 PN W0200121796-A2.
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-US25892.
 XX
 PR 21-SEP-1999; 99US-0155043.
 XX
 PA (GBV) GENETICS INST INC.
 XX
 PI Ling V, Dunussl-Joannopolulos K;
 XX

DR WPI: 2001-244938/25.
P-PSDB: AAB67711.

XX New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT immune response and reducing the proliferation of a tumour cell -
XX

PS Claim 1; Fig 1; 195pp; English.

XX The present sequence encodes a murine GL50-1 polypeptide. GL50
CC molecules are antigens on the surface of antigen presenting cells,
CC which costimulate T cell proliferation and bind to costimulatory
CC receptor ligands on T cells. GL50 modulating agents are used to
CC modulate an immune response in a subject. GL50 polypeptides are used
CC to modulate T cell costimulation, and to reduce the proliferation of
CC a tumour cell. Diseases that can be treated using GL50 molecules are
CC graft-versus-host disease, autoimmune disease, allergies, acquired
CC immune deficiency syndrome (AIDS), and viral infections. The GL50
CC molecules can be used in vaccines. GL50 polynucleotides can be used
CC to locate gene regions associated with genetic disease, in tissue
CC typing, and in forensic identification of a biological sample.

Sequence 2718 BP; 703 A; 709 C; 661 G; 645 T; 0 other:

Query Match 100.0%; Score 966; DB 22; Length 2718;
Best Local Similarity 100.0%; Pred. No. 1.3e-297;
Matches 966; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGCAGCTAAAGTGCCTCTTTTGTGTCTGGGAACGAGCGCTTTGGAAAG 60
DB 67 ATGCAGCTAAAGTGCCTCTTTTGTGTCTGGGAACGAGCGCTTTGGAAAG 126
OY 61 CTCATGTTTCTAGCGGGTCTTTCTGTCTGTCTGCTTCTGCTGTCTGAGCAGC 120
DB 127 CTCATGTTTCTAGCGGGTCTTTCTGTCTGTCTGCTTCTGCTGTCTGAGCAGC 186
OY 121 CTCGTGTGCTCTCTGACAGACTGAATGCGTGCAATGTTGGGCGCAATGTGTCTC 180
DB 187 CTCGTGTGCTCTCTGACAGACTGAATGCGTGCAATGTTGGGCGCAATGTGTCTC 246
OY 181 AACTGATGAGCCCGCAGAGCGCATTTCAACTGAGTGTCTGATGTCATTTGGCAA 240
DB 247 AACTGATGAGCCCGCAGAGCGCATTTCAACTGAGTGTCTGATGTCATTTGGCAA 306
OY 241 ATCGAAGAACCCAGAAAGTTTCGCTGACTACTGCTTCTTACAGTCTCCAGGATCAAT 300
DB 307 ATCGAAGAACCCAGAAAGTTTCGCTGACTACTGCTTCTTACAGTCTCCAGGATCAAT 366
OY 301 GTGACAGTTCTCTACAAGAAAGGGGCCATCTGCTCCCTGAGTCCATGAAGAGGTAAAC 360
DB 367 GTGACAGTTCTCTACAAGAAAGGGGCCATCTGCTCCCTGAGTCCATGAAGAGGTAAAC 426
OY 361 TTCTCTCTGACTGAAGATGTCACCCCTCAGAGATACCAGAGATTCACATCCGGGTA 420
DB 427 TTCTCTCTGACTGAAGATGTCACCCCTCAGAGATACCAGAGATTCACATCCGGGTA 486
OY 421 TTTATGAATACAGCCACAGAGTTAGTCAAGATCTTGAAGAGGTGTCAGGCTGCTGTG 480
DB 487 TTTATGAATACAGCCACAGAGTTAGTCAAGATCTTGAAGAGGTGTCAGGCTGCTGTG 546
OY 481 GCGAGCAAACTTAGTACCTGTCATCAGCACTCTGATAGCTCCAAACCGGGCCAGGAA 540
DB 547 GCGAGCAAACTTAGTACCTGTCATCAGCACTCTGATAGCTCCAAACCGGGCCAGGAA 606
OY 541 CGTACCTACAGCTGCATGTCACAGATGGCTACCCAGAGCCCAACCTGATTGATCAAC 600
DB 607 CGTACCTACAGCTGCATGTCACAGATGGCTACCCAGAGCCCAACCTGATTGATCAAC 666
OY 601 ACAAGCGACAATAGCCTAATATAGACAGCGCTCTGACAGAAATACACTGTCTACTTGAACAAG 660
DB 667 ACAAGCGACAATAGCCTAATATAGACAGCGCTCTGACAGAAATACACTGTCTACTTGAACAAG 726
OY 661 TTGGGCTGTATGATGATGTAATCAGCATTAAGGCTCCCTTGACATCTGTGGGAGTGT 720

DB 721 TTGGGCTGTATGATGATGTAATCAGCATTAAGGCTCCCTTGACATCTGTGGGAGTGT 786
OY 721 CTGTCTGCTGTAGAAATGTGGCTCTCCACGAGAACATCAGATAGCCAGGACGAA 780
DB 787 CTGTCTGCTGTAGAAATGTGGCTCTCCACGAGAACATCAGATAGCCAGGACGAA 846
OY 781 AGTTTCACCTGGAATATACACAAGAACCCACAGAAACCCACAAATATAGTTAAAGTC 840
DB 847 AGTTTCACCTGGAATATACACAAGAACCCACAGAAACCCACAAATATAGTTAAAGTC 906
OY 841 CTGTGCTCCGCTCTGCTGTACTGGCGAGCGCATTCGTTCTTATCATATATACGA 900
DB 907 CTGTGCTCCGCTCTGCTGTACTGGCGAGCGCATTCGTTCTTATCATATATACGA 966
OY 901 CGCAGCGTCCCGACCGAAGTATAGAGCCCAAGACTGTACCTGAACTTACAGAC 960
DB 967 CGCAGCGTCCCGACCGAAGTATAGAGCCCAAGACTGTACCTGAACTTACAGAC 1026
OY 961 CACGCC 966
DB 1027 CACGCC 1032

RESULT 4
AAAF79920
ID AAF79920 standard; DNA; 1759 BP.
XX
AC AAF79920;
XX
DT 11-JUN-2001 (first entry)
XX
DE Nucleotide sequence of a murine GL50-2.
XX
KW GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
KW acquired immune deficiency syndrome; AIDS; vaccine; SS.
XX
OS Mus musculus.
XX
FH
FT CDS
FT
FT Location/Qualifiers
CDS 1..1044
FT /tag= a
FT /product= "GL50"
XX
XX WO200121796-A2.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000MO-US25892.
XX
PR 21-SEP-1999; 99US-0155043.
XX
PA (GENY) GENETICS INST INC.
XX
PI Ling V, Dunussi-Joannopoulos K;
XX
XX WPI: 2001-244938/25.
XX P-PSDB: AAB67712.
XX
XX New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT immune response and reducing the proliferation of a tumour cell -
PT
PS Claim 1; Fig 2; 195pp; English.

The present sequence encodes a murine GL50-2 polypeptide. GL50
CC molecules are antigens on the surface of antigen presenting cells,
CC which costimulate T cell proliferation and bind to costimulatory
CC receptor ligands on T cells. GL50 modulating agents are used to
CC modulate an immune response in a subject. GL50 polypeptides are used
CC to modulate T cell costimulation, and to reduce the proliferation of
CC a tumour cell. Diseases that can be treated using GL50 molecules are
CC graft-versus-host disease, autoimmune disease, allergies, acquired
CC immune deficiency syndrome (AIDS), and viral infections. The GL50

CC molecules can be used in vaccines. GL50 polynucleotides can be used
 CC to locate gene regions associated with genetic disease, in tissue
 CC typing, and in forensic identification of a biological sample.

XX Sequence 1759 BP; 461 A; 506 C; 365 G; 427 T; 0 other;

Query Match 99.0%; Score 956.8; DB 22; Length 1759;
 Best Local Similarity 99.8%; Pred. No. 8.8e-295;
 Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACAGCTAAAGTGTCCCTGTTTGTGCTTGTGGAAACGAGCAGCCTGTTTGGAAAG 60
 |||||||
 DB 1 ATGACAGCTAAAGTGTCCCTGTTTGTGCTTGTGGAAACGAGCAGCCTGTTTGGAAAG 60
 QY 61 CTCACATGTTCTAGCGGGTCTTTCTGGCTTGCTGTGTTCTTCTGCTGCTTGGAGC 120
 |||||||
 DB 61 CTCACATGTTCTAGCGGGTCTTTCTGGCTTGCTGTGTTCTTCTGCTGCTTGGAGC 120
 QY 121 CTCTGCTGCTCTCTGACAGACTGAAGTGGTGGCAATGGTGGCAAGTGGTGGCTC 180
 |||||||
 DB 121 CTCTGCTGCTCTCTGACAGACTGAAGTGGTGGCAATGGTGGCAAGTGGTGGCTC 180
 QY 181 AGCTGATTTGACCCCGACAGACGCCATTTTCACATTGAGTGTCTATTTGGCAA 240
 |||||||
 DB 181 AGCTGATTTGACCCCGACAGACGCCATTTTCACATTGAGTGTCTATTTGGCAA 240
 QY 241 ATGGAAGAACCCAGAAATTTGGTGGTACTTACTGCTTACAGTCTCGAGGATCAAT 300
 |||||||
 DB 241 ATGGAAGAACCCAGAAATTTGGTGGTACTTACTGCTTACAGTCTCGAGGATCAAT 300
 QY 301 GTGGACAGTTCTTACAGAAACAGGGGCGCATCTGCTCGTGGACATCGAAGAGGGTAA 360
 |||||||
 DB 301 GTGGACAGTTCTTACAGAAACAGGGGCGCATCTGCTCGTGGACATCGAAGAGGGTAA 360
 QY 361 TTCTCTCTGACTGAGAAATGTACCCCTCAGAGATACCAGAGATTTACATGCCGGTGA 420
 |||||||
 DB 361 TTCTCTCTGACTGAGAAATGTACCCCTCAGAGATACCAGAGATTTACATGCCGGTGA 420
 QY 421 TTTATGAAATACAGCCACAGATTTAGTCAAGATCTTGGAGAGGTGGTCAAGCTGCTG 480
 |||||||
 DB 421 TTTATGAAATACAGCCACAGATTTAGTCAAGATCTTGGAGAGGTGGTCAAGCTGCTG 480
 QY 481 GCAGCAAACTTCTGATACCTGTATCAGACCTGTGATAGTCCAAACCGGGCCAGGAA 540
 |||||||
 DB 481 GCAGCAAACTTCTGATACCTGTATCAGACCTGTGATAGTCCAAACCGGGCCAGGAA 540
 QY 541 CGTACCTACACCTGATGCTTCCAAAGATGGCTTACCAGAGCCCAACCTGTATTGGATCAAC 600
 |||||||
 DB 541 CGTACCTACACCTGATGCTTCCAAAGATGGCTTACCAGAGCCCAACCTGTATTGGATCAAC 600
 QY 601 ACAAGGACAATAGCTTAATAGACAGCGCTCTCGAGAAATACACTGTCTACTTGAACAAG 660
 |||||||
 DB 601 ACAAGGACAATAGCTTAATAGACAGCGCTCTCGAGAAATACACTGTCTACTTGAACAAG 660
 QY 661 TTGGGCTGTATGATGTAATCAGACATTTAAGGCTCCCTTGGACATCTGCTGGGGATGTT 720
 |||||||
 DB 661 TTGGGCTGTATGATGTAATCAGACATTTAAGGCTCCCTTGGACATCTGCTGGGGATGTT 720
 QY 721 CTGTGCTGCTAGAGATGTGCTCTCCACAGACATCACTAGCATTTAGCCAGGAGAA 780
 |||||||
 DB 721 CTGTGCTGCTAGAGATGTGCTCTCCACAGACATCACTAGCATTTAGCCAGGAGAA 780
 QY 781 AGTTTACAGTGAATAACACAAAGAACCCACAGAAACCCACAAATATAGCTTAAAGTTC 840
 |||||||
 DB 781 AGTTTACAGTGAATAACACAAAGAACCCACAGAAACCCACAAATATAGCTTAAAGTTC 840
 QY 841 CTGTGCTGCTGCTGCTGATGAGGGGCGAGGGCAATGCTTCTTCATCATATACAGA 900
 |||||||
 DB 841 CTGTGCTGCTGCTGCTGATGAGGGGCGAGGGCAATGCTTCTTCATCATATACAGA 900
 QY 901 CGCAGCGTGTCCACGAGAGCTATACAGAGCCAGAGCTGTACAGCTTGAAGTACAGAG 960
 |||||||
 DB 901 CGCAGCGTGTCCACGAGAGCTATACAGAGCCAGAGCTGTACAGCTTGAAGTACAGAG 960

RESULT 5
 AAF79942
 ID AAF79942 standard; DNA; 1830 BP.

XX AAF79942;
 XX 11-JUN-2001 (first entry)

XX Nucleotide sequence of mGL50-mig2am fusion protein.

XX GL50: antigen; antigen presenting cell; T cell proliferation; tumour;
 KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
 KW acquired immune deficiency syndrome; AIDS; vaccine; ss.

OS Synthetic.
 OS Mus musculus.

XX Key Location/Qualifiers
 FH CDS 26..1716

FT /*tag= a
 FT /note= "contains introns"
 FT 26..842
 FT /*tag= b
 FT 843..951
 FT /number= "1"
 FT /tag= c
 FT /number= "1"
 FT 952..1281
 FT /*tag= d
 FT /number= "2"
 FT 1282..1393
 FT /tag= e
 FT /number= "2"
 FT 1394..1716
 FT /*tag= f
 FT /number= "3"

XX WO200121796-A2.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US25892.

XX 21-SEP-1999; 99US-0155043.

XX (GEMV) GENETICS INST INC.

XX Ling V, Dunussi-Joannopoulos K;

XX WPI; 2001-244938/25.

XX P-PSDB; AAB67719.

XX New isolated nucleic acid encoding a GL50 polypeptide for modulating a
 PT immune response and reducing the proliferation of a tumour cell -

XX Disclosure; Fig 29A; 195pp; English.

XX The present sequence encodes a fusion protein, comprising murine GL50
 CC (mg50) and murine IgG2a (migG2A). The fusion protein is used in the
 CC course of the invention. The specification describes GL50 polypeptides.
 CC GL50 molecules are antigens on the surface of antigen presenting cells,
 CC which costimulate T cell proliferation and bind to costimulatory receptor
 CC ligands on T cells. GL50 modulating agents are used to modulate an immune
 CC response in a subject. GL50 polypeptides are used to modulate T cell
 CC costimulation, and to reduce the proliferation of a tumour cell. Diseases
 CC that can be treated using GL50 molecules are graft-versus-host disease,
 CC autoimmune disease, allergies, acquired immune deficiency syndrome
 CC (AIDS), and viral infections. The GL50 molecules can be used in vaccines.
 CC GL50 polynucleotides can be used to locate gene regions associated with
 CC genetic disease, in tissue typing, and in forensic identification of a
 CC biological sample.

Db 635 ACCTTCACTTGCATGTCCAGATGGCTACCCAGAGCCCAACTGTATGTGATCAACAG 694
QY 604 AGGACAAATACCTTAATAGACAGCGCTCTGCAGATAAAGTGTCTACTTGAACAGTTG 663
Db 695 ACGGACAAATACCTTAATAGACAGAGCTCTGCAGATAAAGTGTCTACTTGAACAGTTG 754
QY 664 GGCGTGTATGATGTAATACAGACATTAAGGCTCCCTTGGACATCTCGTGGGATGTTCTG 723
Db 755 GGCGTGTATGATGTAATACAGACATTAAGGCTCCCTTGGACATCTCGTGGGATGTTATC 814
QY 724 TGTCTGCTAGAGATGTGGCTCTCCACAGAACATCACTACATTTAGCCAGAGCAAAAGT 783
Db 815 TGTCTGCTAGAGATGTGGCTCTCCACAGAACATTTACTATATACAGCCGGGAGATAGT 874
QY 784 TTTCACTGGA---AATAACACAAGAACCCACAGAGAAACCAATTAATAGTTAAAGTC 840
Db 875 TTTCACTGGAAGACAGACAGAGAGCCACAGAGAAATCCACAGAGAGCTTACAAAGGTC 934
QY 841 CTGTGCCCCGCTTGTGCTATGCTGGGCAAGCGCATTCCTTCTTCATCA-----TA 894
Db 935 CTTTTCTACGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 994
QY 895 TACAGATGCAAGCAGC---CGTCCCAACGAAAGTATACAGAGCCCAAGAGCTTGAAG 951
Db 995 TACAGATGCAAGCAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1054
QY 952 CTTCACAGACCAAGCC 966
Db 1055 CTCACAGACCAATTC 1069

RESULT 7

AAAA3831 standard: cDNA; 545 BP.

AAAA3831:

21-AUG-2000 (first entry)

Mouse secreted expressed sequence tag SEQ ID NO:406.

Human; mouse; chicken; rat; secreted expressed sequence tag; SESR;
expressed sequence tag; EST; probe; chemotactic; proliferative;
immunomodulatory; haematopoietic; chemokine; analgesic; haemostatic;
thrombolytic; antiinflammatory; cytoskeletal; antibacterial; antifungal;
antiviral; antidiabetic; neuroprotective; vulnary; antiparkinsonian;
cerebroprotective; osteoprotective; antidepressant; gene therapy;
vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
Klinefelter's syndrome; burn; osteoporosis; osteoarthritis;
central nervous system disorder; Alzheimer's disease; stroke;
Parkinson's disease; Huntington's disease; coagulation disorder;
haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
tumour; infection; depression; psoriasis; ss.

Mus musculus.

MO200021991-A1.

20-APR-2000.

15-OCT-1999: 99WO-US24206.

15-OCT-1998: 98US-0104436.

(GENY) GENETICS INST INC.

Jacobs K, McCoy JM, Lavallee ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman MR;

WPI: 2000-317938/27.

XX

PT Isolated polynucleotides, and encoded proteins, comprising secreted
PT expressed sequence tags (SESTs), useful for treating various disorders
PT such as autoimmune, infectious, and central nervous system disorders -
PS Claim 1; Page 309; 803pp; English.

XX AAA43426 to AAA45925 represent specifically claimed secreted expressed
CC sequence tags (SESTs), isolated from human, mouse, chicken and rat
CC tissue sources. The SESTs can have a range of activities depending on
CC the tissues they were isolated from. The activities include:
CC chemotactic; proliferative; immunomodulatory; haematopoietic;
CC chemokine; analgesic; haemostatic; thrombolytic; antiinflammatory;
CC cytoskeletal; antibacterial; antifungal; antiviral; antidiabetic;
CC antisthmatic; vulnary; antiparkinsonian; osteoprotective;
CC neurotropic; antiparkinsonian; antipsoriatic; cerebroprotective;
CC anticonvulsant; and antidepressant. The SESTs can be used for gene
CC therapy and in vaccines. The SESTs are useful as probes for the
CC identification and isolation of full-length cDNAs and genomic DNA
CC molecules which correspond to the SESTs. Proteins encoded by the SESTs
CC are useful in assays for determining biological activity and raising
CC antibodies. They may be useful for treatment of autoimmune disorders
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC osteoporosis, osteoarthritis, central nervous system disorders
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
CC disease), tumours, bacterial, fungal or viral infections, depression and
CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
CC in the exemplification of the present invention.

SQ Sequence 545 BP; 117 A; 151 C; 138 G; 138 T; 1 other:

Query Match 46.6%; Score 450.6; DB 21: Length 545;

Best Local Similarity 98.9%; Pred. No. 2.6e-133;

Matches 453; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGACGCTAAGTGTCCCTTTTGTGCTCTTGGAAACAGCGCCTGTTGGAAAG 60
Db 87 ATGACGCTAAGTGTCCCTTTTGTGCTCTTGGAAACAGCGCCTGTTGGAAAG 146
QY 61 CTCGATGTTCTAGCGGGTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 147 CTCGATGTTCTAGCGGGTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 206
QY 121 CTCTGTGCTGCTCTGCGAGAGTGAAGTGTGCAATGTGGGCAAGTGTGCTC 180
Db 207 CTCTGTGCTGCTCTGCGAGAGTGAAGTGTGCAATGTGGGCAAGTGTGCTC 266
QY 181 AGCTGATGACCCCGACAGAGCCATTTCACTTGAAGTGTGCTGCTGCTGCTGCTGCTG 240
Db 267 AGCTGATGACCCCGACAGAGCCATTTCACTTGAAGTGTGCTGCTGCTGCTGCTGCTG 326
QY 241 ATGAAACCCAGAAATTTGCGTACTTACTCTGCTTCAAGTCTCAGAGATCAAT 300
Db 327 ATGAAACCCAGAAATTTGCGTACTTACTCTGCTTCAAGTCTCAGAGATCAAT 386
QY 301 GTGACAGTCTTCAAGAAACAGGGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 387 GTGACAGTCTTCAAGAAACAGGGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 446
QY 361 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 447 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 506
QY 421 TTTATGATACAGCCACAGAGTGTAGTCAAGATCTTGA 458
Db 507 TTTATGATACAGTCAAGAGTGTAGTCAAGATCTTGA 544

RESULT 8

AAA64556 standard: DNA; 864 BP.

XX

AC		AA64556;	
XX			
DT		02-JAN-2001 (first entry)	
XX			
DE		DNA sequence encoding a human B7RP1 polypeptide.	
XX			
KW		CRP1; CD28 related protein-1; B7RP1; B7 related protein-1; T-lymphocyte activation; type I transmembrane protein; T cell activation; T cell proliferation; T-cell mediated disorder; ss.	
KM			
XX			
OS		Homo sapiens.	
XX			
FH		Key	Location/Qualifiers
FT		CDS	1..864
FT			/tag= a
FT			/product= "B7RP1"
FT			/note= "no termination codon given"
FT		sig_peptide	1..48
FT			/tag= b
FT		mat_peptide	49..864
			/tag= c
PX			
PN		WO200046240-A2.	
XX			
PD		10-AUG-2000.	
XX			
PF		27-JAN-2000; 2000WO-US01871.	
XX			
PR		03-FEB-1999; 99US-0244448.	
PR		08-MAR-1999; 99US-0264527.	
XX			
PA		(AMGE-) AMGEN INC.	
PI		Yoshinaga SK;	
XX			
DR		WP1; 2000-543476/49. P-PSDB; AAB08727.	
XX			
PT		Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful in the treatment, prevention and diagnosis of T cell mediated disorders	
PT		-	
PS		Claim 2; Fig 3A; 174pp; English.	
XX			
CC		The present sequence encodes a B7RP1 (B7 related protein-1) polypeptide. The specification also describes a CRP1 (CD28 related protein-1) polypeptide. The polypeptides are involved in T-lymphocyte activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are predicted to be a type I transmembrane protein. The nucleic acids are useful for regulating T cell activation or proliferation in an animal. The polypeptides are useful for treating, preventing ameliorating or diagnosing a T-cell mediated disorder in an animal. They can also be used to identify test molecules that bind to the polypeptides.	
CC			
CC			
XX			
SO		Sequence 864 BP; 197 A; 245 C; 250 G; 172 T; 0 other;	
Query Match	31.0%; Score 299.6; DB 21; Length 864;		
Best Local Similarity	64.8%; Pred. No. 6,1e-85;		
Matches 478; Conservative	0; Mismatches 254; Indels 6; Gaps 2		
89	GTCCTTGATCTGTTCTGTGGCTGTTGAGCAGCCTCTGTGCTCCCTTGCGAGACTGANG	148	
Db			
14	GTCCTGGAAGCTGCTTCCTCGTCTTCAGCAGCCTTGAGACTGATTACTCAAGAAGANG	73	
OY	149 TCGGTGCATATGTTGGGCGACGATGTGCTCAGCTGCATTACCCGCCACAGCGCAT	208	
Db	74 TCAGAGCGGTGTAGGCGACGCGAGCTCAGCTGCGCCTTGCCCTGAAGAACCGCTT	133	
OY	209 TCAACTTGATGCTGTGATGCTATTTGGCAAATGAAAACCAGAGTTTCGGTACCT	268	
Db	134 TTGATTTAATATGATGTTTACGATATTTGGCAAAACAGTAGTCGAAAAACCGTGTACCT	193	
OY	269 ACTACTGCTTACAAGTCTCCAGGAGATCAATGTGACAGTTCCTACAGAAGACAGGGGCC	328	

Db	194	ACCCATCTCCACAGACAGCTCTTGGAAACGTTGGAGCACCCGCTACCGGAACCGAGGCC	253
Qy	329	ATCTGCTCCCTGGACTCCATGACAGCAGGGTACTTCTCTGTACTGTGAAGATGTCCACC	388
Db	254	TGATGTCAACCCGGCGGATGTGGGGGGCACTTCTCCCTGGCTTTCACAGTCAACC	313
Qy	389	CTCAGATACCACAGGATTCACATGACCGGGTATTTATTAATTAACAGCCACAGATTTAGTCA	448
Db	314	CCCAAGACAGACACAAAGTTTCACTGCTGGTGT---TGACCATAATCCCTGGGATTCAGG	370
Qy	449	AGATCTTGGGAAGAGTGTGTCAGGCTGGTGTGGCAGCAAACTTCAGTACACTGTTCATCA	508
Db	371	AGGTTTGACGCTTGAGGTTAACAATGCATGTGGCAGCAAACTTCACAGCTGTCTGTCA	430
Qy	509	GCACCTCTGATAGCTCCACACCCCGGCCAGGACAGTACCTACCTGCATGTCCAAAGATG	568
Db	431	GGGCCCCCACAGCCCTCTCCAGS--ATAGCTCACCTTCACTGATACATCCATTAAGC	487
Qy	569	GCTACCCAGAGCCCAACCTGTATTGGATCAACACAGCAATATACCTAATAGACACGG	628
Db	488	GCTACCCAGAGCCCAACAGTGTACTGATCAATTAAGACGACCAACAGCTGTGACCAAG	547
Qy	629	CTCTGCAGATTAACACTGTCTACTTGAACAAAGTTGGGCTGTATGATTAATCAGACACT	688
Db	548	CTCTGCAGAAATGAACACCGCTCTTTTGAACATGGGGGGCTGTGTAGCAGTGGTAGGCTGC	607
Qy	689	TAAAGCTCTCTTGGACATCTCGTGGGATTTCTGTCTCTCGTGAAGAAATGTTGGCTCTCC	748
Db	608	TGAGATATGCACAGGACCCCGCTGAACATTTGGCTGTCTGCATAGAAGAGTCTTCTGC	667
Qy	719	ACCAGACATCAGTACGATTAGCCAGGACGAGAAAGTTTCACTGGAATTAACACAAGAACCC	808
Db	668	AGCAGAACTCCTAGCTGTGGGCGCAGCCAGAGAAATGACATCGAGAGAGACAGACAAATCA	727
Qy	809	CACAGGAACCCACATTA 826	
Db	728	CAGGAATCCAGTCAGTA 745	
RESULT 9			
ABK87593			
ID	ABK87593	standard; cDNA; 864 BP.	
AC	ABK87593;		
XX			
DI	07-OCT-2002 (first entry)		
XX			
DE	cDNA encoding human B7 related protein-1 (B7RP1) #1.		
XX			
KM	CD28 related protein-1; CPB1; T-lymphocyte costimulatory protein;		
KM	B7 related protein-1; B7RP1; T-cell mediated disorder; hypersensitivity;		
KM	IgE-mediated disorder; allergy; sinus inflammation; immune disease;		
KM	graft survival; immune activation; asthma; cancer gene immunotherapy;		
KM	T-cell dependent B-cell mediated disease; leukaemia; sarcoma; melanoma;		
KM	adenocarcinoma; prostate tumour; lung carcinoma; colon carcinoma; tumour		
KM	viral infection; Hepatitis A virus; autoimmune disorder; psoriasis;		
KM	rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;		
KM	diabetes; immunethrombocytopenic purpura; toxic shock syndrome;		
KM	bone marrow; organ transplantation; inflammatory bowel disease;		
KM	allosensitisation; blood transfusion; graft vs. host disease; human;		
KM	gene; ss.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	1..864		
FT	/*tag= a		
FT	/product= "B7RP1"		
FT	/note= "B7 related protein-1"		
FT	/partial		
FT	/note= "No stop codon given"		
XX			


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Db      37  GTCTGGAGTCTCTTCTCTCTCTTTCAGCAGCCTTCAGCTGATCTACAGAGAAAGAG 96
Qy      149  TCGGTGCAATGTGTGGAGCAATGTGTGCTCAGCTGATTCAGTCCACAGCCGACAT 208
Db      97  TCAGAGCAATGTGTAGCAGCAGCTGAGCTCAGCTGCGCTTCCCTGAGAGAGCCGTT 156
Qy      209  TCAACTGAGTGGTCTATGTCTATTTGGCAATTCGAAACCCAGAGTTTGGTGACT 268
Db      157  TTGATTTAAATGATGTTTACGTATTTGGCAACCAAGTGAAGTGAACCCGTGTACCT 216
Qy      269  ACTACCTGCTTCAAGTCTCAGGATCAATGTGAGCAAGTTCCTCAACAGAGGAGCC 328
Db      217  ACCACATCCACAGAGAGCTCCTTGGAAACGTGACGCGCTACCGGAAACGAGCC 276
Qy      329  ATCTGCTCCGAGCTCAGTCAAGAGCAGGTTAATCTCTCTGTGATCAGTGAAGATGTCACC 388
Db      277  TGAATGACCGCGCGGCTGCTGCGGCGAGCTTCTCCCTGCGCTTGTTCACAGTCAACC 336
Qy      389  CTCAGGATACCCAGAGATTCACATGCGCGGTATTTATGAATACAGCCACAGAGTTAGTCA 448
D      337  CCCAGAGCAGAGAGAGTTTCACTGCTGTGT---TGAGCCAAATCCCTGGGATTCAGG 393
Qy      449  AGATCTGGAAGAGTGTGTGAGCTGCTGCTGAGCAAACTTCAGTACACCTGTCTATCA 508
Db      394  AGGTTTGAAGCTTGAGGTTTACATGCTGATGTGCAAGCAAACTTCAGCGCGCTGTCA 453
Qy      509  GCACCTCTGATAGCTTCAACCCGCGGCAAGAGTACCTACACCTGATGTCAGAAATG 568
Db      454  GGGCCCCCAGAGCCCTCCAGG---ATGAGCTTCACTTCACTGATCTCAATTAACG 510
Qy      569  GCTACCCAGAGCCCAACCTGATTTGATCAACACAGAGCAATAGCCTAATAGACAGG 628
Db      511  GGTACCCAGAGCCCAACCTGATGATCAATTAACAGAGCAAGCCTGCTGAGACAGG 570
Qy      629  CTCTCAGAAATACCTGCTACTGATGAGCAAGTTGGGCTGTATGATGATTAATCAACAT 688
Db      571  CTCTCAGAAATACCTGCTCTTCTTGAACATGCGGGCTTGTATGAGCTGTGCTGCTGC 630
Qy      689  TAAAGCTCCCTTGGACATCTGCTGGGATGTTCTGCTGCTGAGTGAATGTGCTGCTGC 748
Db      631  TGAGGATGCGACGCGACCCCGAGCTGAACATTTGGCTGTGATGAGACAGCTGCTTTCG 690
Qy      749  ACCGAAATCACTAGCTTATGAGCAGAGCAAAATTTCACTGGAATTAACAAAGAAC 808
Db      691  AGCAGAACTACTGTGTGCGCAGACAGAGAAATGACATCGAGAGAGAGACAAAGATCA 750
Qy      809  CACAGGAAACCCACATA 826
C      751  CAGAGAAATCCAGTCAGTA 768

RESULT 12
AAAG4557
ID      AAAAG4557 standard; DNA: 1294 BP.
AC      AAAAG4557;
XX
XX
XX      02-JAN-2001 (first entry)
XX
XX      DNA sequence encoding a human B7RP1 polypeptide.
XX
XX      CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
XX      T-lymphocyte activation; type I transmembrane protein; T cell activation;
XX      T cell proliferation; T cell mediated disorder; ss.
XX      Homo sapiens.
XX
XX      Key
XX      5'UTR      1..199      Location/Qualifiers
XX      FT      /*tag= a
XX      FT      200..1108
XX      CDS      /*tag= b

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FT      sig_peptide      /product= "B7RP1"
FT      200..247
FT      /*tag= c
FT      mat_peptide      248..1105
FT      /*tag= d

W0200046240-A2.
10-AUG-2000.
27-JAN-2000; 2000MO-US01871.
03-FEB-1999; 99US-0244448.
08-MAR-1999; 99US-0264527.
(AMGE-) AMGEN INC.
Yoshihaga SK;
WPI: 2000-543476/49.
P-PSDB: AAB08729.

PT      Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
PT      in the treatment, prevention and diagnosis of T cell mediated disorders

PS      Claim 2; Fig 12A; 174bp; English.
XX
XX      The present sequence encodes a B7RP1 (B7 related protein-1)
XX      polypeptide. The specification also describes a CRP1 (CD28 related
XX      protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
XX      activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
XX      predicted to be a type I transmembrane protein. The nucleic acids are
XX      useful for regulating T cell activation or proliferation in an animal.
XX      The polypeptides are useful for treating, preventing ameliorating or
XX      diagnosing a T-cell mediated disorder in an animal. They can also be
XX      used to identify test molecules that bind to the polypeptides.

SQ      Sequence 1294 BP; 262 A; 400 C; 392 G; 240 T; 0 other;

Query Match      31.0%; Score 299.6; DB 21; Length 1294;
Best Local Similarity 64.8%; Pred. No. 7.7e-85;
Matches 478; Conservative 0; Mismatches 234; Indels 6; Gaps 2;

Qy      89  GTCTGTGTTGTTTCTGCTGCTGTTGAGCAGCCTTGTGCTGCTGCTGAGACTGAG 148
Db      213  GTCTGTGACTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 272
Qy      149  TCGGTGCAATGTGTGGGCAAGTGTGTGCTCAGCTGATTCAGTCCACAGAGCCATT 208
Db      273  TCAGAGCAATGTGTAGCAGCAGCGAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 332
Qy      209  TCAACTGAGTGGTCTGATGTCTATGTGCAAAATCGAAACCCAGAAAGTTTGGTGACT 268
Db      333  TTGATTTAAATGATGTTTACGATATATGGCAACAGAGTATCCAAACCGTGTGACT 392
Qy      269  ACTACCTGCTTCAAGTCTCAGGATCAATGTGACAGTTCCTTACAAAGAGAGGAGCC 328
Db      393  ACCACATCCACAGAGAGCTCTTGGAAACGTGAGACAGCGCTTACCGGAAACGAGCC 452
Qy      329  ATCTGCTCCGAGCTCAGTCAAGTCAATGTGAGCAAGTTCCTTACAAAGAGAGGAGCC 388
Db      453  TGAATGACCGCGCGGCTGCTGCGGCGAGCTTCTCCCTGCGCTTGTTCACAGTCAACC 512
Qy      389  CTCAGGATACCCAGAGATTCACATGCGGCTATTTATGAATAGAGCCACAGAGTTAGTCA 448
Db      513  CCCAGAGCAGAGAGAGTTCACATGCTGCTGTGT---TGAGCCAAATCCCTGAGTTTCAGG 569
Qy      449  AGATCTGGAAGAGTGTGTGAGCTGCTGCTGAGCAAACTTCAGTACCTGTCTATCA 508
Db      570  AGGTTTGAAGCTTGAGGTTTACATGCTGATGTGAGCAAACTTCAGCGCGCTGTCTCA 629
Qy      509  GCACCTCTGATAGCTTCAACCCGCGGCAAGAGTACCTTACACCTGATGTCAGAAATG 568

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Key	Location/Qualifiers
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51..113	
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WO200164704-A1.	
07-SEP-2001.	
02-MAR-2001; 2001WO-US06769.	
02-MAR-2000; 2000US-O186519.	
(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.	
Chen L;	
WPI: 2001-514837/56.	
P-PSDB: AAG67292.	
An isolated DNA encoding a h87-H2 polypeptide, useful for treating cancer, AIDS, or autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis or insulin-dependent diabetes mellitus) -	
Example 2; Fig 2A; 50pp; English.	
The present sequence encodes a human polypeptide, designated h87-H2. The h87-H2 polypeptide co-stimulates T cells. The h87-H2 proteins and its variants are generally useful as immune response-stimulating therapeutics. For example, the polypeptides can be used for treatment of disease conditions characterized by immunosuppression, e.g., cancer, AIDS or AIDS-related complex, other virally or environmentally-induced conditions, and certain congenital immune deficiencies. They may also be employed to increase immune function that has been impaired by the use of radiotherapy or immunosuppressive drugs such as certain chemotherapeutic agents, and therefore are particularly useful when given in conjunction with such drugs or radiotherapy. The h87-H2	

CC	inucleic acid and polypeptide can be used to treat conditions
CC	Involving cellular immune responses, e.g., inflammatory conditions
CC	(such as, for example, those induced by infectious agents including
CC	Mycobacterium tuberculosis or M. lepreae), or other pathologic
CC	cell-mediated responses such as those involved in autoimmune diseases
CC	(e.g., rheumatoid arthritis), multiple sclerosis, or insulin-dependent
CC	diabetes mellitus).
CC	
XX	
Seq	Sequence 1453 BP; 306 A; 428 C; 441 G; 278 T; 0 other;
Query Match	31.0%; Score 299.6; DB 22; Length 1453;
Best Local Similarity	64.8%; Pred. No. 8.2e-85;
Matches 478; Conservative	0; Mismatches 254; Indels 6; Gaps 2
QY	89 GTCCTGGTCTGTTCTTGCTCTGTTGACAGCCTCTGTGCTGCTTGCAGAGACTGAAG 148
Db	64 GTCTCTGACGTGCTCTTCTGCTCTTGAAGCAGCCTTGAGCTGTATCTCAGAGAAAGGAAG 123
QY	149 TCGGATGCATAGTGGGACAGCAATGTGTGCTGCTAGTGCATATGACCCCAAGAGCCGCAAT 208
Db	124 TCAGAGGAGATGTAAGCAGAGAGAGTGTGAGACTGACGTGCTGCTGCTGTAAGAGCCGTT 183
QY	209 TCAACTTGAAGTGTCTGTATGTCTATTGGCAATTCGAAAAACCGAAGTTTGGGTACTT 268
Db	184 TTGATTAAATGATGTTATGTTATGCTATATGGCAACACAGTAGATGCAAAACCGGTGACCT 243
QY	269 ACTACGCGCTTCAAGTCTCCAGGGATCAATGTGGACAGTTCCTTCAAGAAACGAGGCCC 328
Db	244 ACCACATCCCAAGCAAGAACAGCTCTTGAAAAACCTGACAGCCGCTACCGAACCGAGCCC 303
QY	329 ATCTGTCCCTGACACTCATAGAAAGACAGGATTAACCTCTGTACCTGAAAGATGTACACC 388
Db	304 TGATGTACCGGCGCGGACATGTGCGGGGGGACCTTCTCCCTGGCTTGTCAACGTACACC 363
QY	389 CTCAGATACCAAGAGATTACATGCCGGGTATTATGAATACAGCCACAGATTAGTCA 448
Db	364 CCCAGAGCAGACAGAAAGTTTCACTGCTGTGTGT--TGAGCCCAATCCCGGAGATTCCAG 420
QY	449 AGATCTTGGAAAGGTGGTCAAGGCTCCGTGGACAGCAACTTCAGTACACTGTCACTCA 508
Db	421 AGGTTTGAAGCGTTGAGATTACATGTCATGTGGACAGCAACTTCAAGCGTCCGTGTCTA 480
QY	509 GCACCTCTGATAGTCCAAACCCGGGACAGAAAGTACCTACCTGTGATGTCCAAAGATG 568
Db	481 GCGCCCCCCACAGCCCTCCCAAG--ATGAGCTCACCTTCACGTGATCATCTAAAG 537
QY	569 GGTACCAAGAGCCCAACCTGTATTGGATCAACACAAGGACATATAGCTAATAGACAGG 628
Db	538 GCTACCCCAAGGCCCAACGTTACTGATCAATAAAGACGACCAACAGCCTGTGCGACAGG 597
QY	629 CTCTGAGAAATTAACACTGTCTACTTGAACAAAGTTGGGCTGTATGATATGTAATCAGCAAT 688
Db	598 CTTCTGAGAAATGACAACCGCTTCTTGAACATGCGGGGCTTGTATACGTGGTCAAGCTGTC 657
QY	689 TAAAGCTCCCTTGGACATCTCTGCGGGATGTTCTGTGCTGCTAGAGATGTGCTCTCC 748
Db	658 TTAGAGATGCAAGACCCCAAGCGTGAACATTTGGCTGCTGATATAGAAACATGCTTCTGC 717
QY	749 ACCAAGATCATCTAGCAATTAGCAGGAGAGAAAGTTTCACTGAGAAATTAACAAAGAAC 808
Db	718 ACCAAGATCATCTGCGGACCGACAGACAGAAATGACATGTGGAGAGAGACAAAGATCA 777
QY	809 CACAGAAACCCACATA 826
Db	778 CAGAGAAATCCAGTCAGTA 795
RESULT 15	
AAS00423	
ID	AAS00423 standard; cDNA: 1548 BP.
AC	
XX	AAS00423;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 17, 2002, 01:50:50 ; Search time 1399.38 Seconds
(without alignment)
11179.834 Million cell updates/sec

Title: US-09-728-421D-6

Sequence: 1 atgcagcctaaggttcctcctg.....ttgaactacagaccagcgc 966

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_estrc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_estl3:*
12: gb_estl4:*
13: gb_estl5:*
14: gb_estl6:*
15: em_estfun:*
16: em_estfun2:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467.2	48.4	872	12	BF580455 602097224
2	465	48.1	663	10	BB612511 BB612511
3	454	47.0	694	10	BB227026 BB227026
4	434	44.9	661	10	BB638093 BB638093
5	410	42.4	538	9	AI614037 AI614037
6	316.6	32.8	577	10	BB637248 BB637248

7	298	30.8	962	9	AL560774
8	297	30.7	440	9	AA510455
9	296.4	30.7	1083	14	BM923293
10	281.6	29.2	978	13	BM543561
11	219	22.7	816	13	B1488470
12	164	17.0	496	10	AM753046
13	163	16.9	486	10	AM377686
14	151.6	15.7	422	14	R23544
15	147.2	15.2	476	12	BE776710
16	130	13.5	663	10	BB637811
17	113.8	11.8	448	10	AM377683
18	102.4	10.6	363	12	BE721193
19	63.8	6.6	771	13	BI911468
20	57.8	6.0	475	12	BE603992
21	53.2	5.5	674	13	BI393131
22	39.4	4.1	417	10	AM445859
23	39.4	4.1	936	17	CNS04667
24	39.2	4.1	837	12	BE730328
25	38.8	4.0	518	9	AI788059
26	38.2	4.0	578	9	AI788059
27	37.6	3.9	589	9	AJ449399
28	37.6	3.9	836	12	BM863018
29	37.2	3.9	555	17	AZ713664
30	37	3.8	710	9	AJ453546
31	37	3.8	718	9	AJ446897
32	37	3.8	785	9	AJ447809
33	36.8	3.8	593	9	AJ448922
34	36.8	3.8	601	9	AJ449097
35	36.8	3.8	616	9	AJ450379
36	36.8	3.8	618	9	AJ449599
37	36.8	3.8	628	13	BM489980
38	36.8	3.8	645	13	BM439415
39	36.8	3.8	691	9	AJ450167
40	36.8	3.8	702	9	AJ449834
41	36.8	3.8	717	9	AJ448384
42	36.8	3.8	725	9	AJ451418
43	36.8	3.8	730	9	AJ446899
44	36.8	3.8	734	9	AJ452616
45	36.8	3.8	788	9	AJ446332

ALIGNMENTS

RESULT 1
BF580455
LOCUS
DEFINITION
602097224F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4217333 5',
mRNA sequence.
BF580455
ACCESSION
BF580455.1 GI:11654167
VERSION
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
NIH-MGC <http://mgs.nci.nih.gov/>.
1 (bases 1 to 872)
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM9795 row: P column: 06
High quality sequence start: 2
High quality sequence stop: 670.
Location/Qualifiers

FEATURES

Source	1. . 872	/organism="Mus musculus"	/strain="FVB/N"	/db_xref="taxon:10090"	/clone="IMAGE:4217333"	/clone_11b="NCI CGAP Co24"	/lab_host="DH10B (T1 phase-resistant)"	/note="Organ: colon; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."
BASE COUNT	199 a	251 c	218 g	204 t				
ORIGIN								
Query Match	48.4%	Score 467.2	DB 12	Length 872				
Best Local Similarity	86.0%	Pred. No. 2.5e-132						
Matches 614	Conservative	0	Mismatches 83	Indels 17	Gaps			
OY	1	ATGCAGCTAAAGTGTGCCCTGTTTGTGTC- TTGGGACACAGCAGCCGTGTGGAGAA	59					
	157	ATGCAGCTAAAGTGTGCCCTGTTTGTGTC- TTGGGACACAGCAGCCGTGTGGAGAA	216					
OY	60	GCTCATGTTTCTACGGGTTCTTTTGTGCTTGTGCTGTTCTGTGCTGTGACAG	119					
Db	217	GCTCATGTTTCTACGGGTTCTTTTGTGCTTGTGCTGTTCTGTGCTGTGACAG	276					
OY	120	CCTGTGCTGCTGCTGTGCAGACATGAAATCGTGCATGAGTGGGAGACATGTGCT	179					
Db	277	CCTGTGCTGCTGCTGTGCAGACATGAAATCGTGCATGAGTGGGAGACATGTGCT	336					
OY	180	CAGTGCATGACCCCCACAGAGCCATTTCACTTGAAGTGTGATGTCTA- TTGGC	238					
Db	337	CAGTGCATGACCCCCACAGAGCCATTTCACTTGAAGTGTGATGTCTA- TTGGC	396					
OY	239	AAATGAAACCCCAAGTTTGGTGAATCTACTGCTGCTTCAAGTCCAGGATGA	298					
Db	397	AAATGAAACCCCAAGTTTGGTGAATCTACTGCTGCTTCAAGTCCAGGATGA	456					
OY	299	ATGTGACAGTTCCTACAAAGACAGGGCCATCTGTCCCTGGACTCCATGAAGCAG	358					
Db	457	ATGTGACAGTTCCTACAAAGACAGGGCCATCTGTCCCTGGACTCCATGAAGCAG	516					
OY	359	ACTTCTCTCTGACCTGGAAGATGTACACCC- TCAAGGATACCCAGAGTTCACATGCCG	417					
Db	517	ACTTCTCTCTGACCTGGAAGATGTACACCC- TCAAGGATACCCAGAGTTCACATGCCG	576					
OY	418	GTAATTATG- AATACAGCCACAG- AGTAGTCAAGATCTTGGAA- -GAGGTGTGACGC	472					
	577	GTAATTATGAAATACAGCCACAGCAGTAGTAGTACAGATCTTGGAGAGAGGTGTCCAGGC	636					
OY	473	TGCGGTGTGGACCA- -AACTTCAGTACACCTGTCAATCAGACCTCTGTACTGTCA	526					
Db	637	TGCGGTGTGGACCACTTACAGTTTAACTTCAGTTCATCAGACCTCTGTACTGTCA	696					
OY	537	ACCCGGCCAGAGAGTACTACATCCTCCTGATCCCAAGAGGCTACACAGGCCAAC	586					
Db	697	ACCCGGCCAGAGAGTACTACATCCTCCTGATCCCAAGAGGCTACACAGGCCAAC	756					
OY	587	TGTATTGATCAACACAGAGGACATAGCTTATATAGACAGG- -CTCTGCAGATTAACA	643					
Db	757	TGTATTGATCAACACAGAGGACATTAATATATAGACAGGCTTGTGCAGAAATATAC	816					
OY	644	CTGTCTACTTGAAAGTGGGCTGTATGATGATATACAGCATTAGAGCTCC	697					
Db	817	TGCTTACTTGAAAGTGGGCTGTATGATGATATACAGCATTAGAGCTCC	870					
RESULT 2								
LOCUS	BB612511	663 bp	mRNA	linear	EST 26-OCT-2001			
DEFINITION	BB612511	RIKEN full-length enriched, 0 day neonate skin Mus						
ACCESSION	BB612511	musculus cDNA clone 4652416J18 5', mRNA sequence.						

VERSION	B8612511.1	GI:16453443
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
AUTHORS	1 (bases 1 to 663)	
TITLE	ARKAWA,T., CARINCI,P., FUKUDA,S., FURUNO,M., HANAGAKI,T., HARA,A., HIRAMOTO,K., HORTI,F., ISHII,Y., ITO,M., KAWAI,T., KONNO,H., KODA,M., KOYA,S., MATSUYAMA,T., MIYAKAWA,A., NOMURA,K., OHNO,M., OKAZAKI,Y., OKIJO,T., SAITO,R., SAKAI,C., SAKAI,K., SANO,H., SASAKI,D., SHIBATA,K., SHINAGAWA,A., SHIRAKI,T., SOGABE,Y., SUZUKI,H., TAGAMI,M., TAGAWA,A., TAKAHASHI,F., TAKEDA,Y., TANAKA,T., TOYA,T., MURAMATSU,M. and HAYASHIZAKI,Y.	
JOURNAL	RIKEN Mouse ESTs (Arkawa,T., et al. 2001)	
COMMENT	Unpublished (2001) Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gscc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carinci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carinci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamamaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.	
FEATURES	Location/Qualifiers	
SOURCE	1..663	
	/organism="Mus musculus"	
	/strain="C57BL/6J"	
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	/clone="4632416J18"	
	/clone_lib="RIKEN full-length enriched, 0 day neonate skin"	
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	/dev_stage="0 day neonate"	
	/lab_host="DH10B"	
	/note="Site_1: Sali. Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'	
	GAAAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'] cDNA was prepared by using Trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization	

QY	528	CCGGGCGCAGGAAGCTACTACTACCTGGATGTCGCAAGATGGCTACCCAGACCCAACT	587	
Db	61	CCGGGCGCAGGAAGCTACTACTACTGTCATGTCGCAAGATGGCTACCCAGACCCAACT	120	
QY	588	GTATTGGATCAACACACACGAGACATAGCTTAATAGACAGCGCTCTGCAGAAATACACTGT	647	
Db	121	GTATTGGATCAACACACGAGACATAGCTTAATAGACAGCGCTCTGCAGAAATACACTGT	180	
QY	648	CTACTTGAACAAAGTGGGCGCTGTATGATGTATTCAGCAATTAAGGTCCTTGGACATC	707	
Db	181	CTACTTGAACAAAGTGGGCGCTGTATGATGTATTCAGCAATTAAGGTCCTTGGACATC	240	
QY	708	TCTGTGGGATGTTCTGTGTGTGTAGAGAAATGGCTCTCCACCAAGCAATCATAGACAT	767	
Db	241	TCTGTGGGATGTTCTGTGTGTGTAGAGAAATGGCTCTCCACCAAGCAATCATAGACAT	300	
QY	768	TAGCCAGCAGCAAAATTTCTACTGCGAAATTAACCAAAAGAACCCACAGAGAAACCAATTA	827	
Db	301	TAGCCAGCAGCAAAATTTCTACTGCGAAATTAACCAAAAGAACCCACAGAGAAACCAATTA	360	
Db	828	TGAGTAAAGATCCTGTGCTGCCGCTCTTGCCTTGTACTGGGCGAGGCGCATTTGTTCTCT	887	
QY	361	TGAGTAAAGATCCTGTGCTGCCGCTCTTGCCTTGTACTGGGCGAGGCGCATTTGTTCTCT	420	
Db	888	CATCATATACAGACGACGCGCTCCCGACCGAAGCTATACAGG	929	
Db	421	CATCATATACAGACGACGCGCTCCCGACCGAAGCTATACAGG	462	
RESULT 4	BB638093	661 bp	mRNA linear	EST 26-OCT-2001
LOCUS	BB638093	RIKEN full-length enriched, 3 days neonate thymus	Mus	
DEFINITION	musculus cDNA clone A630008D12 5', mRNA sequence.			
ACCESSION	BB638093			
VERSION	BB638093.1	GI:16473797		
KEYWORDS	EST.			
SOURCE	house mouse			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 661)			
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Himoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,T., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasakawa,T., Shibata,K., Shinagawa,A., Shirai,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takehashi,F., Takeeda,Y., Tanaka,T., Toya,T., Muramatsu,M., and Hayashizaki,Y.			
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp URL: http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagl,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,T., Okazaki,Y., Muramatsu,M., Inoue,Y., Kikuta,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara			

,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shindagawa,A., Saito,T., Kiyosawa,H., Yamanahe,I., Aizawa,
'K.', Fukuda,S., Hara,A.I., Itoh,M., Kawal,J.J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

e mouse tissues.

location/Qualifiers

1 . 661
/organism="Mus musculus"
/db_xref=taxon:10090"
/clone="A630008D12"
/clone_lib="RIKEN full-length enriched, 3 days neonate
thymsus"
/tissue_type="thymsus"
/dev_stage="--3 days neonate"
/lab_host="DH10B"

/note=Site.1: SalI; Site.2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGGAGAAGATCCACAGACTCTTTTGTTCCTTTTTTTTTVVN 3'] , cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGAGAAGATTCTCGATAATTAATTAATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHl. Vector : a modified pbluescript KS(+) after bulk exisition from LambdaFLC T."

BASE COUNT 140 a 191 c 165 g 165 t
ORIGIN

Query Match 44.9%; Score 434; DB 10; Length 661;
Best Local Similarity 96.4% ; Pred. No. 3.7e-122;

Matches 476; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

OY 1 ATGCAGCTAAAGTGTCCTCTTTGGTGTGCTTGGGAACCAGCACCTGTTGGAAGAAG 60
DB 168 ATGCAGCTAAAGTGTCCTCTTTGGTGTGCTTGGGAACCAGCACCTGTTGGAAGAAG 227

OY 61 CTCCATGTTTTCAAGGGGGTCTTTCTGAGTGTGCTGTTCTCTGCTGTTGAGCAGC 120
DB 228 CTTCCATGTTTCAAGGGGGTCTTTCTGAGTGTGCTGTTCTCTGCTGTTGAGCAGC 287

OY 121 CTCTGTGCTGCCCTGFCAGAGACTGAAGTCGSTGCAATGTGTGGCAGACAATGTGGTCTC 180
DB 288 CTTCTGTGCTGCCCTGFCAGAGACTGAAGTCGSTGCAATGTGTGGCAGACAATGTGGTCTC 347

OY 181 AGCTCATTTGACCCCACACAGAGSCCATTTCAAAGTAGGGGCTGTATGTCATTGGGCA 240
DB 348 AGCTCATTTGACCCCACACAGAGSCCATTTCAAAGTAGGGGCTGTATGTCATTGGGCA 407

OY 241 ATCGAAAACCCACGAAG -TTTGCGTACTTACTACCTGCTGCTGACTGCATGAMCAGGATCA 299
DB 408 ATCGAAAACCCACGAAGTTTGGTGCTACTTACTGCTGCTTNCAGTGTCCAAGGATCA 467

OY 300 TTGTGACAGTTTCCTAACAGAACAGGGGCCATCTGTCCCTGAGCTGCATGAMCAGGATCA 359
DB 468 TTGTGACAGTTTCCTAACAGAACAGGGGCCATCTGTCCCTGAGCTGCATGAMCAGGATCA 527

OY 360 CTCTCTCTGTATCCGTGAAGATGTACCCCTGAGATACCA -GGAGTTCACATG -CCGG 417
DB 528 CTCTCTCTGTATCCGTGAAGATGTACCCCTGAGATACCAAGGAGATGTACATGTCCCGG 587

QY	418	GTATTATGAATGACCGACGAGTTAGTCACATCTCTGGAAGAAGTGTCAGAGCTCCGT	477
Db	588	GTTATTATGATTCAGCCGCCAGATTAGTCACATCTCTGGAAGAAGTGTCAGAGCTCCGT	647
QY	478	GTGGCAGCAACTT	491
Db	648	GTTGCACCAACTT	661
RESULT 5			
LOCUS	A1614037		
DEFINITION	A1614037	538 bp mRNA linear EST 21-APR-1996	
ACCESSION	V932FE09.X1	Soares.mammary_gland_NBMKG Mus musculus cDNA clone	
VERSION	IMAGE:663001.5	similar to TR:075144 075144 KIAA0653 PROTEIN ;	
KEYWORDS	RNA sequence.		
SOURCE	A1614037.1	GI:4623204	
TAXONOMY	EST.		
	house mouse.		
	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1	(bases 1 to 538)	
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
	MGI:507169		
	This read is a RESEQUENCE of a previously sequenced mouse clone		
	This read has been verified (found to hit its original self in the		
	correct orientation)		
	Possible reversed clone: similarity on wrong strand		
	Seq primer: -40RP from Glibco		
	High quality sequence stop: 345.		
FEATURES	location/Qualifiers		
source	1..538		
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	/lab_host="DH10B"		
	/note="Organ: mammary gland; Vector: pUT73D-Pac (pharmacia		
	RI; 1st strand cDNA was primed with a Not I - oligo(dt)		
	primer 15'		
	TGTTACCAATCTGAATGGGAGCGCGCGCAATGTTTTTTTTTTTTTTTTTTTTTT		
	T 3']; double-stranded cDNA was ligated to Eco RI		
	adaptors (Pharmacia), digested with Not I and cloned into		
	the Not I and Eco RI sites of the modified pUT73 vector.		
	RNA provided by Dr. Minoru Ko, Wayne State Univ. library		
	constructed and normalized by Benito Soares and M.Fatima		
	Bonafido."		
BASE COUNT	111 a 155 c 129 g 142 t	1 others	
ORIGIN			
Query Match	42.4%	Score 410; DB 9; Length 538;	
Best Local Similarity	96.3%;	Pred. No. 8.4e-115;	
Matches	419; Conservative	0; Mismatches 16; Indels 0; Gaps 0;	
QY	1	ATGCACTAAAGGTGTCCTGTTTGTGTCTCTTGGGAACAGCAGCTGTTGGAGAAG	60
Db	104	ATGCAGCTAAAGTGTCCTGTTTGTGTCTCTTGGGAACAGCAGCCTGTTGGAGAAG	163
QY	61	CTCCATGTTTCTACGGGTTCTTTTCGGTTTGTGCTCTTCTTCTGCTGCTGTGAGCAGC	120

Db	Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	164	CTCCATGTTTTCAGCGGGTCTTTTCTGGTCTGGTCTGTTCTGCTGTTGAGACAC								
Qy	121	CTCTGTGCTGCCCTCTCCACAGACTGAAGTCGGGCAATGGGGACGAATGGTGGTC								
Db	224	CTCTGTGCTGCCCTCTCCACAGACTGAAGTCGGGCAATGGGGACGAATGGTGGTC								
Qy	181	ACGTCGATTGACCCGCCACAGAGCCGCAATTTCAACTTGAAGTGGTCTATGTTATGGCAA								
Db	284	ACGTCGATTGACCCGCCACAGAGCCGCAATTTCAACTTGAAGTGGTCTATGTTATGGCAA								
Qy	241	ATCGAAAACCCAGAAAGTTTCGGTGAATTAATCTACCTGCTTTACAAAGTCTCCAGGATCAAT								
Db	344	ATCGAAAACCCAGAAAGTTTCGGTGAATTAATCTACCTGCTTTACAAAGTCTCCAGGATCAAT								
Qy	301	GTGGACAGTTCCTTACAAAGAACAGGGGGCCATCTGTGCTGGAGTCCATGATGAAGAGGTATAC								
Db	404	GTGGACAGTTCCTTACAAAGAACAGGGGGCCATCTGTGCTGGAGTCCATGATGAAGAGGTATAC								
Qy	361	TTTCTCTGTGTACCTGAAGAATGTCAACCCCTCAGATATCCAGAGTTCATCATGCGCGGTA								
Db	464	TTTCTCTGTGTACCTGAAGAATGTCAACCCCTCAGATATCCAGAGTTCATCATGCGCGGTA								
Qy	421	TTTATGAATACAGCC 435								
Db	524	TTTATGAATACAGTC 538								
RESULT 6										
LOCUS	BB637248									
DEFINITION	BB637248 RIKEN full-length enriched, adult male aorta and vein Mus									
ACCESSION	BB637248									
VERSION	BB637248.1									
KEYWORDS	EST.									
SOURCE	house mouse.									
ORGANISM	Mus musculus.									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
AUTHORS	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
	1 (bases 1 to 577)									
	Arkawa,T., Carinici,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,									
	Himono,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Komno,H., Kouda,									
	M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,									
	Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,									
	D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,									
	Togami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,									
	Muramatsu,M. and Hayashizaki,Y.									
	RIKEN Mouse ESTs (Arkawa,T., et al. 2001)									
	Unpublished (2001)									
	Contact: Yoshihide Hayashizaki									
	Laboratory for Genome Exploration Research Group, RIKEN Genomic									
	Sciences Center(GSC), Yokohama Institute									
	The Institute of Physical and Chemical Research (RIKEN)									
	1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan									
	Tel: 81-45-503-9222									
	Fax: 81-45-503-9216									
	Email: genome-res@gs.riken.go.jp,									
	URL: http://genome.gsc.riken.go.jp/									
	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh									
	M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.									
	Normalization and subtraction of cap-trapper-selected cDNAs to									
	prepare full-length cDNA libraries for rapid discovery of new									
	genes. Genome Res. 10 (10), 1617-1630 (2000)									
	wagi,K., Fujiwaka,S., Inoue,K., Togawa									

D 532 GGGCCCCCAGACGCCCTCCAGG---ATGAGCTACCTTCAGCTGATCATCATTAACG 588
Q 569 GCTTACCCAGAGCCCACTGATTGATCAACACAGGACATAGCCTTAATAGACACGG 628
D 589 GCTTACCCAGAGCCCACTGATTGATCAACACAGGACATAGCCTTCCTGACACGAT 648
Q 629 CTCGACGAATTAACGTCTACTTGAACAAAGTTGGGCTCTATGATGATATCAGCAT 688
D 649 CTCGACGAATTAACGTCTACTTGAACAAAGTTGGGCTCTATGATGATATCAGCAT 708
Q 689 TAAGGCTCCCTTGGACATCTCTGGGATGTTCTGCTGCTGATAGAAATGTGCTCTCC 748
D 709 TGAGAGTGGACGACGCCACCCAGCCTGAACATGTGCTGCTGATAGAACGCTCTTCTGC 768
Q 749 ACCAAGAACATCTAGCATTAAGCCAGCAGAAAGTTTCACTGGAATTAACAAAGAAC 808
D 769 AGCGAAGCTGACTGCTGGGCGCAGAGAAATGACATCGAGAGAGACAAAGATCA 828
Q 809 CACAGAAACCCACATTA 826
D 829 CAGGAATCCAGTCAGTA 846

RESULT 8
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LOCUS IMAGE:863081.5, mRNA sequence.
ACCESSION AA510455
VERSION AA510455.1 GI:2248309
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 440)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maria M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:307169
Seq primer: -28m13 rev2 ET from Amerisham
High quality sequence stop: 408.

FEATURES
source

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Location/Qualifiers
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/strain="C57BL/6J"
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/clone="IMAGE:863081"
/clone_lib="Soares_mammary_gland_NbMWG"
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/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia
RI: 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5']
TGTACCAATCTGAACTGGAGCGCCGCAATGTTTTTTTTTTTTTTTTTTTTT
T 3'] double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into

BASE COUNT
ORIGIN

Query Match 30.7%; Score 297; DB 9; Length 440;
Best local similarity 99.7%; Pred. No. 4.9e-80;
Matches 308; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Q 1 ATGAGCTTAAGTGTCCCTGTTTGTCTCTTGGGAAACAGGACGCTGTTGGAAGAAG 60
D 133 ATGAGCTTAAGTGTCCCTGTTTGTCTCTTGGGAAACAGGACGCTGTTGGAAGAAG 192
Q 61 CTCACGTTTCTAGCGGGGTTCTTTCTGCTTGTGCTGCTGCTGCTGCTGCTGCTG 120
D 193 CTCACGTTTCTAGCGGGGTTCTTTCTGCTTGTGCTGCTGCTGCTGCTGCTGCTG 251
Q 121 CTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
D 252 CTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Q 181 AGCTGATGACCCCGACAGCCGATTCACCTTGAAGTGTGCTATTTGGCAA 240
D 312 AGCTGATGACCCCGACAGCCGATTCACCTTGAAGTGTGCTATTTGGCAA 371
Q 241 ATCGAAGAACCCAGAGTTTGGTGTACTTACTGCTGCTTCAAGTGTCCAGGATCAAT 300
D 372 ATCGAAGAACCCAGAGTTTGGTGTACTTACTGCTGCTTCAAGTGTCCAGGATCAAT 431
Q 301 GTGACACGT 309
D 432 GTGACACGT 440

RESULT 9
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LOCUS AGENCOURT_6625900 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5758883
DEFINITION 5', mRNA sequence.
ACCESSION BM923293
VERSION BM923293.1 GI:19373672
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC <http://mgi.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLAM12803 row: 9 column: 12
High quality sequence stop: 741.

FEATURES
source

1..1083
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/clone="IMAGE:5758883"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo

QY 509 GCACCTTGATAGTTCACCGGGGCGAGMAAGTACCTACCTGCATGTTCAGAAATG- 568
 Db 505 GCGGCCCCACAGACCCCTCCAGG---ATGACCTACCTCAAGTGTCAATCAATAACG 621
 QY 509 GCTTACCAGAGGCCCAACCTGTATTGGATCAACAACAGGACAAATAGCTTAATTAACACGG 628
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 QY 689 TAAAGCTCCCTTGG-ACATCTCGTGGGGATGTTCTGTGCTCCTAGAGAAATGTGGCTTC 747
 Db 742 TGAGAGATCGCACGMAACCCCCAGCGTGAACATTTGGCTCTGCATTAAGAGAACGTCCTTCTG 801
 QY 748 CACCAAGAACTCACTAGCAATTAGCCAGGCGAAGAAATTTCACTGGAATTAACACAAAGAC 807
 Db 802 CAGAGAGAACTGACTCTCGGCAAGCCAGCAAGAAATTAAGCATTCGGAGAGAGACACCAATC 861
 QY 808 CCACAGGAACCC 819
 Db 862 CCGGAGAAATCC 873

RESULT	11
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LOCUS	BI488470
DEFINITION	BI488470 Homo sapiens mRNA EST 28-AUG-2001 603020971c1 NIH-MGC_114 Homo sapiens cDNA clone IMAGE:5121864 5' , mRNA sequence.
ACCESSION	BI488470
VERSION	BI488470.1 GI:15327698
KEYWORDS	EST .
SOURCE	human. .S
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euarchontes; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
TITLE	Contact: Robert Strausberg, Ph.D.
JOURNAL	
COMMENT	

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FEATURES
source
1. 816
High quality sequence stop: 790.
Location/Qualifiers
Plate: LRAM1479 row: m column: 17
http://image.llnl.gov
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
DNA Sequencing by: Incyte Genomics, Inc.
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Issue Procurement: Life Technologies, Inc.
CNA Library Preparation: Life Technologies, Inc.

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BASE COUNT	166 a	258 c	230 g	162 t
ORIGIN				

Query Match	22.78;	Score 219;	DB 13;	Length 816;
Best Local Similarity	65.98;	Pred. No. 7.1e-56;		

	Matches	395;	Conservative	0;	Mismatches	195;	Indels	9;	Gaps	5
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Db	147	GTCCTTGAACTGCTCTTCTCGCTCTTCAGCAGCCCTTGACTGATCTCAAGSAGAAGG	206							
QY	149	TGCGTGCATAATGGGGCACCAATGTGSGTCTCAGCTGCATTGACCCTCCACAGACCCATT	208							
Db	207	TGAGAGCGATGCTGAGCACCAGCTGAGACTCAGCTGCCCTTGGCCCTTGAAGGAAGCCGTT	266							
QY	209	TCACAATGAGTGGCTGTATGTCTATTGGCAATGCAAAAACCCAGAAAGTTTGGTGACTT	268							
Db	267	TGTATTTAATGATGTTTACGATATATTGGCAAACCAAGTAGTCGAAAAACCGTGTGACTT	326							
QY	269	ACTACTGCGCTTACAAGTGTCCAGGGATCATATGTGACAGTTCCTCAACAAGACAGGGCC	328							
Db	327	ACCAATATCCACAGAAACAGCTCTTGGAAAAAGTGGACAGCGCTTACCGAACCAGAGCCC	386							
QY	329	ATCTGTCCCTGGATCAGCATGAGCAGAGGGTAATCTCTCTGTACTGTGAAGATGTCACCC	388							
Db	387	TGATGTACACGGCGCCGACATGCTGCGGGGAGCACTTCTCCTGTGGCTTGTCAACGTCACCC	446							
QY	389	CTCAGGATACCCAGAGATTACACATCCCGGGTATTTATGAATACAGCCACAGAGTAFTCA	448							
Db	447	CCCAAGAGAGCAGAGAAGTTTCACTCCTGCTGTGT--TAGGCCAATCCCTGGGATTTCCAGG	503							
QY	449	AGATCTTGGGAAGAGTGTGTGAGGCTGTGCTGTGTGGCAGCAAATCTTCAGTACACCTGTATCA	508							
Db	504	AGGTTTTTGAAGCTTGAGGTTACACTGTCATGTGTGGCAGCAAACTTCAGCGTGCCTCGTCFCA	563							
QY	509	GCACCTCTGATAGTCCCAACCCGGGCCAGSAAAGTACTTACACCTGATGCAATGTCGA-AGAT	567							
Db	564	GCGCCCCCACAAGCCCTCTCCAGG---ATGAGCTCACCTTACAGGTACATTCATTAAMAC	620							
QY	568	GCGTACCCAGAGCCCAACCTGTATTGTGATCAACAACAAGCAGCAATTA-GCCTAATAGACAC	626							
Db	621	GCGTACCCCAAGGCCCAACGCTGACTGATCATTAAGACGAGCAACACGCCCTGTGCTGACCA	680							
QY	627	GGCCTGTGAGAAATAACATGCTCTACTTGTGACA-AGTTGGCCTGTATGATGTAAATCAAGC	684							
Db	661	GGCCTGTGAGAAATACACCGTCTTCTTGTGMAATATGCGGGGCTGTGTATGACGCTGTGCTAC	739							

RESULT	12
LOCUS	AM753046
DEFINITION	PM2-CT0238-290999-001.g01 CT0238 Homo sapiens cDNA, mRNA sequence.
ACCESSION	AM753046
VERSION	EST.
KEYWORDS	human.
SOURCE	

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 496)
AUTHORS	Dias, Nercio, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M. R., Naga, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Metsukum, A., Bala, G. S., Simpson, D. H., Brustein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704982
Fax: +55-11-2707001
Email: aslmpson@ludwig.org.br

DEFINITION Y34612.r1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:34465 5', mRNA sequence.

ACCESSION R23544
VERSION R23544.1 GI:778432
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 422)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Merra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 2783
High quality sequence stops: 364 Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 2783 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 364.
Location/Qualifiers

FEATURES
source
1..422
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/clone_lib="Soares infant brain INIB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Laifmid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAGAAATTCGGCGCGGCGGAGAAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Laifmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 100 a 122 c 121 g 78 t 1 others

Query Match 15.7%; Score 151.6; DB 14; Length 422;
Best Local Similarity 67.3%; Pred. NO. 3e-35;
Matches 230; Conservative 0; Mismatches 109; Indels 3; Gaps 1;

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1 CAAACTTCAGTACACCTGTATCGACACCTGTATGTATCCACCGGCGGAGACCTA 57
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545 CCTACACCTGCATGTCCAGAAATGCTACACGAGCCCAACCTGTATGTATCAACAA 604
|||||
58 CCTTCACCTGTATCCATTAAGAGGCTACCCGAGCCCAACCTGTATGTATCAATA 117
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605 CGGACAAATAGCTTAATAGACAGGCTGTGCAATTAACACTGTCTACTTGAACAATTGG 664
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118 CGGACAAACAGCTCTGTGACGAGGCTGTGCAATTAACACTGTCTTGAACATGGCGG 177
|||||
665 GCCGTATGATGATTAATAGACCAATTAAGGCTCTTGACATCTCGTGGGATGTTCTGT 724
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178 GCTTGTATGAGTGTGCTGTGAGGATGCAAGGAGCCCGGCTTGAACATTTGGCT 237
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725 GCTGCGTAGAAGATGTGCTCTCCACGAGAACTAGCTAGCTTAGCGAGCAAAAGTT 784
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Db 238 GCTGCATGAGAGAGCTGCTTGTGACAGAGAACTGACTGTGGGACGACGAGAAATG 297

Qy 785 TCACTGGAATTAACAAAGAACCCACGAGAAACCCACATA 826
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Db 298 ACATCGAGAGAGAGACAAAGATCACAGAAATCCAGTACATA 339
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RESULT 15
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LOCUS BF776710
DEFINITION 287583 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF776710
VERSION BF776710.1 GI:12124610
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 476)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Pette, G., Holt, I., Karameycheva, S., Liang, F., Quackenbush, J. and Keeler, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred v0.980904.e. Vector identified by cross_match with the -m1nscore 18 and mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGAG
Plate: 92 row: J column: 22
Seq primer: AATTAGGTGACACTATAG.

FEATURES
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/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendoneous muscle, and fetal longissimus muscle."

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Query Match 15.2%; Score 147.2; DB 12; Length 476;
Best Local Similarity 66.4%; Pred. No. 7.1e-34;
Matches 247; Conservative 0; Mismatches 113; Indels 12; Gaps 2;

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23 TTGAGAGTGTGACAGCTCGTGTGACAGCAACTTCACTATCATCAGAGCTG 80
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514 TCTGATGATCTCAACCGGCGGACGAGTCTTACACCTGATCCCAAGATGGCTAC 573
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Qy 574 CCAGAGCCCAACCTGTATTGATCAACAAAGGACATATGACAGCGGCTCTG 633
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Db 134 CCGGGCCCAATGTGTACTGATCAACAAAGGAGCAACAGCGTGTGACAGGCGCTG 193
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QY 634 CAGAAATACACTGTCTACTTGAACAAGTGGCCGTATGATGATATCAGCACATTAAG 693
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Db 254 ATCGGGCGAAACCCCGCATGTCAACGTGGGCTGTGATGAGAAATGTGTCTACACCAG 313
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QY 754 AACATCACTAGCATTAGCCAGGAGAAAGTTTCACTGGAATTAACACAAAGAACCCACAG 813
    |||||
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Job time : 1406.38 secs

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142 GTCTCTGGAGCTCTCTCTCTCTCTTCACGACCCCTTCAGAGCTGATACAGAGAAAGGAAG 201
0Y 149 TCGCTGCATATGCTGGGAGCAATGTGGTGCCTACACTGCATTTGACCCCAACAGACCATTT 208

Db	202	TCAGAGCGATGTGAGGACGAGCGACTGGAGCTCAAGCTCGCTTGCCCTCGAAGAAAGCCGTT	261
QY	209	TCACACTTGAGTGTGTCGTATGTCTATTGGCAAAATCGAAAAACCAAGAGTTTCGGTACATT	268
Db	262	TTGATTTTAAATGATTTTACCTATATTGGCAAAACCACTGATGTGAAAAACCGTGTACACT	321
QY	269	ACTACCTCCCTTACAAAGTCTCCAGGATTCATGTGGAACGACGTACTCTCTTCAACAAAGGAGGCC	328
Db	322	ACCACATCCCAACAAACAGCTCTCTTGGAAAAACGTGGACACGCGCTACCGGAACCGAGCC	381
QY	329	ATCTGTCCCTTGAGTCCATGAGCAAGGAGTACTTCTCTGTATCACTGGAAGATGTCAACC	388
Db	382	TGATGTCAACGGCCGCGGATGCTCGCGGGGCGACTCTCTCCGTGCGCTTGTCAAGTCACCC	441
QY	389	CTCAGGATACCCAGAGGTGCACATGCGCGGGTATTTATGATPACAGCCACAGAGTTAGTCA	448
Db	442	CCCAAGAGAGCAAGAAAGTTTCACTGCTGGTGT--TGAGCAATCCCTTGGATTCACAG	498
QY	449	AGATCTTGGAAGAGGTGTGTCAGGCTGCGGTGTGGCAGCAAACTTCAGTACACTGTGATCA	508
Db	499	AGGTTTATGAGGRTTGTAGGTTTACATGCTGATGTGGCAGCAAACTTCAGCGTCCGTCGTCA	558
QY	509	GCACCTCTGATAGCTCCACACCCGGGGCCAGAAAGTACCTACCTGCTGATGTCCAAAGATG	568
Db	559	GGCGCCCCCAAGGCCCTCCACAG--ATGAGCTCACTTCAGCTGTACATTCATAAACG	615
QY	569	GCTACCCAGAGCCCAACCTGTATTGGATCAACACAGCAAGCAATAGCCTAATAGACAGG	628
Db	616	GCTACCCAGAGCCCAACGCTGTACTGTACATTAAGAGGAAACAGCCTGCTGTGACCAAG	675
QY	629	CTCTGCAGATTAACACTGTCTACTTTGAACAAAGTTGGGCTGTGATGATGTATACACAT	688
Db	676	CTCTGCAGATTAACACCGCTCTTCTTGAACAAATGCGGGCTGTGTAAAGCAGTGTGACGCTGC	735
QY	689	TAAAGCTCCCTTGGACATCTCTGTGGGAGTGTCTGTGCTGGGTGAGAAATGTGGACTGTC	748
Db	736	TGAGGATGCGCAGGAGACCCCGACGCTGAACATTTGCGTCTGCTGATGAGAAAGTGTCTGTC	795
QY	749	ACCAGAACATCACTAGCATTTAGACGCGAGCAAAAGTTTCACTGGAATTAACCAACAAGAC	808
Db	796	AGCAACAACCTGACTGTGCGGACGACAGCAAGAAATGACATCGAGAGAGACAAAGATCA	855
QY	809	CACAGAAACCCACATA	826
Db	856	CAGAGATTCAGTCAGTA	873

RESULT 2

9-789-561-64

Sequence 64, Application US/09789561

Patent No. US20020064818A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: 52 Human secreted proteins

FILE REFERENCE: P2043P1

CURRENT APPLICATION NUMBER: US/09/789,561

CURRENT FILING DATE: 2001-02-22

PRIOR APPLICATION NUMBER: PCT/US00/24008

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: 60/152,317

PRIOR FILING DATE: 1999-09-03

PRIOR APPLICATION NUMBER: 60/152,315

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 194

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 64

LENGTH: 2751

TYPE: DNA

ORGANISM: Homo sapiens

US-09-789-561-64

Query Match 31.0%; Score 299.2; DB 10; Length 2751;

Best Local Similarity 64.6%; Pired. No. 7.5e-85;

	Matches	477:	Conservative	1:	Mismatches	254:	Indels	6:	Gaps	2:
QY	89	GTCTTGTTGTC	TTTTTGGCTTGTCTGCTGTTGAGCAGCCCTGTGTCCTCTCGACAGACTGAAG	148						
Db	231	GTCTTGAGCAT	TGCTCTCCCTCTTCACAGAGCCTTCGACCTGATCTACAGGAAGAAG	290						
QY	149	TGGGTGCAT	TGCTGGGACGACATGTGTCCTCAGCTGCACTTAGTACCACACAGCCCAATT	208						
Db	291	TGAGAGCCAT	TGTTAAGCACGCCAGCGAGAGCTAGCTAGCTGGCCCTTGAAAGAACCCGTT	350						
QY	209	TCACTTGAGT	GGTCTGTATGTCTATTGGCAATGGAANAACCCACAAGTTTCGGTGACTT	268						
Db	351	TGTATTTAA	TATATGATTTATACGTATATTGGCAACACAGTGAAGTCGAAACCCGTGGACTT	410						
QY	269	ACTACTGGCTTA	CACAGTCCAGGAAATGTGAGACAGTTCCTACAAAGACAGAGGGCC	328						
Db	411	ACCACTATCC	CACAGAACAGCTCTCTTGGAANAAGCTGACAGCCGCTACCCGGAACCCAGCCC	470						
QY	329	ATCTGTCCCTG	ACATTCATGAAGCAGGATTAACCTTCTCTGTACTGAAGAATGTACACC	388						
Db	471	TGATGTACAC	CGGCGCGGACCTGCTGGGGGAGCATTTCTCCCTGCGCTTGTCCAAGCTACACC	530						
QY	389	CTCAGATAC	CCAGAGSTTCACATGCGCGGTATTATGAATPACGACCAAGAGTTAGTCA	448						
Db	531	CCCAGAGCAG	AAGATGTTCACTGCTGTGTGT--TGAGCCAAATCCCTGGGATTCAGG	587						
QY	449	AGATCTTGGAA	AGGTGGTGTGAGGCTGCGCTGTGGCAGCAACCTTCAGTACACCTGTATCA	508						
Db	588	AGGTTTGTAG	CRHTGTGAGTTTACATGTCATGTGGCAGCAAACTTCAGCGCTGGCTGTCA	647						
QY	509	GCACCTCTAT	AGCTTCCAAACCCGGGCGCAGGAACGTACACACCTGACATGTCAGAAATG	568						
Db	648	GGGCCCCC	CACAGCCCTCCCAAG--ATGAGCTCAACCTTCAGTGTATCATTAACG	704						
QY	569	GGTACCCAG	AGCCCAACTGTATTGGATPAACACAAGGACACATAGCCTAATATGACAGG	628						
Db	705	GCTACCCAG	CGCCCAACGTGTACTGATATAAAGAGGGAACAACAGCCGTGCGACCAAG	764						
QY	629	CTCTCGAAT	PAACTGTGTACTGTAGACAAGTTGGGCTGTATGATGTAACTACGACACT	688						
Db	765	CTCTGAGAT	PAAACCCGCTTCTTGMACTCGGGGCTTGATGACGTTGTCACGCTGC	824						
QY	689	TAAAGCTCC	CTTGGACATGCGTGGGAGATGTTCTGCTGCTGAGAAATGTGGCTCTCC	748						
Db	825	TGNGATTC	CCAGGAGCCCAAGCTGTACATTTGGCTGTGTCATAGAGAAGCTGTCTTCC	884						
QY	749	ACCAGAACT	CACTAGCATTAACGACAGAGAAAGTTTCACTGGAATTAACACAAAGACC	808						
Db	885	AGCAGAACT	CACTGTCGCGACGACAGAGAAATGACATCGAGAGAGACAAAGATCA	944						
QY	809	CACAGAA	ACCACATA 826							
Db	945	CAGAGAT	CCAGTCACTA 962							
RESULT 3										
US-09-764-853-210										
; Sequence 210 Application US/09764853										
; Patent No. US20020090672A1										
; GENERAL INFORMATION:										
; APPLICANT: Rosen et al.										
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies										
; FILE REFERENCE: PIZ06										
; CURRENT APPLICATION NUMBER: US/09/764,853										
; CURRENT FILING DATE: 2001-01-17										
; Prior application data removed - consult PALM or file wrapper										
; NUMBER OF SEQ ID NOS: 939										
; SOFTWARE: PatentIn Ver. 2.0										
; SEQ ID NO 210										
; LENGTH: 2616										
; TYPE: DNA										
; ORGANISM: Homo sapiens										
US-09-764-853-210										

PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1655
LENGTH: 1879
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1_N17300
US-09-917-800A-1655

Query Match 3.5%; Score 33.4; DB 10; Length 1879;
Best Local Similarity 51.7%; Pred. No. 2.3;
Matches 76; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

OY 504 CATTGACCTGATGATGCTCAACCGGCGGAGGAGTCAACCTGATGCTCAAC 563
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
DB 726 CACCACTGCTCCAAACAAAGTCAATGACCCCTGGAAAGGACCTTCTCGAGGAGAA 667
OY 564 GAATGCTACCCAGACGCCAACCTGATGATGATCAACACAGGACAATAGCCTAATAGA 623
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
DB 666 ACAGGCTCCCGGATTCGGGCTTCTTACATGATGATCTGATGACACGAGTGCATAT 607
OY 624 CAGGCTCTGCAATATCACTGCTCTA 650
|| || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
DB 606 ACCACCTTTCAGAAATGACATATCCA 580

RESULT 8

US-09-783-590-61/c
Sequence 61, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16,2C1
CURRENT APPLICATION NUMBER: US/09/783,590
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61
LENGTH: 236
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (11)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (130)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (135)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (191)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (200)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (201)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-61

Query Match 3.4%; Score 33.2; DB 10; Length 236;
Best Local Similarity 61.7%; Pred. No. 0.78;
Matches 50; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 756 CATCTAGCATTTAGCCAGACAGATTTCATGTAATTAACAAAGAACCCACAGCA 815
|| || || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
DB 219 CCTCACTCATTTAGTCANNAGGAAATTAATTAATTAACAGTAATTAACCTCTACA 160
OY 816 ACCCAACAATATGAGTTAAA 836
|| || || || |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
DB 159 AATCTATAGATGAGTTAAA 139

RESULT 9

US-09-960-352-15003
Sequence 15003, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 15003
LENGTH: 229
TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: unsure
LOCATION: (63)...(64)...(67)...(69)...(70)...(96)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 64-LIB3058-040-Q1-K1-H8
US-09-960-352-15003

Query Match 3.4%; Score 33; DB 10; Length 229;
Best Local Similarity 60.0%; Pred. No. 0.88;
Matches 54; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY 752 AGAATCATCTAGCATGAGCAGAGAAAGTTCACTGGAATTAACAAAGAACCCAC 811
|| || || || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
DB 94 AGNAAAAACCAAGATTTAGCAGAAATTAATAAATTAATTAACCAAAAAACCAAA 153
OY 812 AGGAACCCACAAATATGAGTTAAAGTCC 841
|| || || || || || || || || || || || || || || || || || || || || ||||
DB 154 ACAGAAAGGAAAAAAGCAAGCAAGCC 183

RESULT 10

US-09-960-352-9888/c
Sequence 9888, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.

```

;
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.

```

Query Match	3.48;	Score 32.4;	DB 10;	Length 873;
Best Local Similarity	46.28;	Pred. No. 3.1;		
Matches 148; Conservative	0;	Mismatches 166;	Indels 6;	Gaps 1;

RESULT 15
US-10-002-775-1

Sequence 1, Application US/10002775
Patent No. US20020102651A1

GENERAL INFORMATION

APPLICANT: Gordon Freeman

APPLICANT: Vassilki Bou

APPLICANT: Tatyana Chernova

APPLICANT: Nelly Malenkovich
TITLE OF INVENTION: NOVEL B7-A VORPOUR NO AND NO2S

FILE REFERENCE: GNN-004ADY

CURRENT APPLICATION NUMBER: IIS/10/003 775

CURRENT FILING DATE: 2001-11-02

PRIOR APPLICATION NUMBER: IIS 09/644-934

PRIOR FILING DATE: 2000-08-23

PRIOR APPLICATION NUMBER: 60/150,390

PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

LENGTH: 9

TYPE: DNA

ORGANISM: *Homo sapiens*

NAME/KEY: 0000

NAME/KEY: CDS
LOCATION: (59) (703)

LOCATION: (59)..(793)

T-C// - 200 - 0T 50

Query Match	3.48;	Score 32.4;	DB 12;	Length 968;
Best Local Similarity	46.28;	Pred. No. 3.3;		
Matches 148; Conservative	0;	Mismatches 166;	Indels 6;	Gaps 1;

Oy 100 TTCCTGACGCTCTTTAGACAGCCTCTGTCTGCTCTGCTGAGACATGAAAGTGGGTGCATG 150
 Db 92 TACTGGCAATTGCTGAACGCATTACTCTCAAGGTTCTCCCAAGGACCTATATATGGTGAAG 150
 Oy 160 GTGGGCAGCAATGTGTGTCTCAGCTGCATTGACCCCCAGAGGCCATTTCAACTTGAGT 210
 Db 152 TATGTATACCAATATACCAATTGAAGGCAAAATTTCCAGTAGAAAAACAATTATGACCTGGCT 210
 Oy 220 GGTCTGTATGCTATTGTGGCAATGCAAAACCAGAAAGTTGCGAGCTTACTACCTGCT 270
 Db 212 GCATTAATTGTCTATTGGGAATGGAGATGAAGAACATT-----ATTCAATTTGTCTCAT 265
 Oy 280 TACAGTCTCCAGGAGATCAATGTGACACAGTTCTCTACAGAAACAGGSGCCATCTGTCCCTG 330
 Db 266 GGAGGGAAGACCTGAAGGTTTACACATATGTGCTACAGACAGAGGGCCCGCTTTGAAG 335
 Oy 340 GACTTCATGAAGCAGGAGTAACCTTCTCTGTACTGAAAGATGTACACCCCTCAGGATACC 390
 Db 326 GACCAAGCTCTCCCTGGGAATGTGTCACTTCAGATTCACAGATGTGAATATTCAGAGATGCA 385
 Oy 400 CAGGAGTTCACATCCCGGT 419
 Db 386 GGGGTGTACCCCTGCATGAT 405

Search completed: November 17, 2002, 06:44:58
Job time : 139.702 secs

[illegible]

```

: LOCATION: (840)
: OTHER INFORMATION: The polymorphism of a T to a C at this position
: OTHER INFORMATION: has appeared in one individual.
: FEATURE:
: NAME/KEY: mutation
: LOCATION: (947)
: OTHER INFORMATION: The missense mutation from a G to a T occurs at
: OTHER INFORMATION: this position in a BFNc family.
: FEATURE:
: NAME/KEY: allele
: LOCATION: (678)
: OTHER INFORMATION: This position is polymorphic for C or T.
: FEATURE:
: NAME/KEY: allele
: LOCATION: (750)
: OTHER INFORMATION: This position is polymorphic for T or C.
: FEATURE:
: NAME/KEY: allele
: LOCATION: (1089)
: OTHER INFORMATION: This position is polymorphic for G or C.
: FEATURE:
: NAME/KEY: allele
: LOCATION: (2598)
: OTHER INFORMATION: This position is polymorphic for T or C.
:
: US-09-177-650-6
:
Query Match
Best Local Similarity 3.4%; Score 33; DB 4; Length 2914;
Matches 95; Conservative 0; Mismatches 85; Indels 1; Gaps 1.
:
OY 281 ACAACATCCCGAGGATGCATATGACACAGTCTCTACAGACAGCGGGCCATGTGCTCCGTGG 340
Db 529 ACTGGCTCCCAAGATGAAATAGAAATAGTCTCCAGTACAGAAAGCCA-GTCTCCCGAG 471
OY 341 ACTCCATGAAGCAGCGGTACTCTCTCTGTAACCTGAAGAAATTCACCCCTCAGATTACCC 400
Db 470 ACAGTCTCATACTCTCTTGATGTGTGTGACAGACAGCCAGATCAAGACACCCAGCAATC 411
OY 401 AGGAGTTACATGCCGGGTATTATGATATACAGCCACAGAGTTAGTCAAGATCTTGGAG 460
Db 410 AGGAACACCAACGCGTGTAAAGCAGCGCCAGCCCGCGGTCTCTCCAGGGGCTGTAG 351
OY 461 A 461
Db 350 A 350
:
RESULT 4
US-09-404-879A-346/C
: Sequence 346, Application US/09404879A
: Patent No. 6468546
: GENERAL INFORMATION:
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: King, Gordon E.
: APPLICANT: Algate, Paul A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.462C2
: CURRENT APPLICATION NUMBER: US/09/404.879A
: NUMBER OF SEQ ID NOS: 393
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 346
: LENGTH: 370
: TYPE: DNA
: ORGANISM: Homo sapiens
:
US-09-404-879A-346
:
Query Match
Best Local Similarity 3.4%; Score 32.6; DB 4; Length 370;
Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
:
368 TGTAACCTGAAGATGTACCCCTCAGATACCCAGAGATTACATGCCGGGTATTATTATGA 427

```

DB 263 TCTACTGCTTATGTACACCAACGACCTATCAGAGGACCTCCAGAGCCGTGATGA 204
QY 428 ATACAGCCACAGATTACTCAAGATCTTGAAGAGGTGCTGAC 470
DB 203 ATAGCAACAGCAATTTCCGGAGAGGCTTGTGAGAACCTGAGAG 161

RESULT 5
US-08-545-809A-2

; Sequence 2, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: GM1
; US-08-545-809A-2

Query Match 3.4%; Score 32.6; DB 3; Length 512;

Best Local Similarity 47.7%; Pred. No. 1.1; Mismatches 104; Indels 0; Gaps 0;

QY 278 CTTACAGTCTCAGGAGTCAATGTGACAGTCTTCAAGAACAGGGGCGCATCTGCCC 337
DB 224 CCGTCAAGGCTTGTGATACACCTTCACGGGTAATATGACCTGGTGCGACAGGCC 283
QY 338 TGGACATCGAAGCAGGGAATCTCTCTGTACTGGAAGATGTCACCCCTCAGAGATA 397
DB 284 CTGCAAGAGGCTTGAAGTGGATGGATGATCAACCTTAACAGTGTGCGACAACTATG 343
QY 398 CCCAGAGTTTACATCCCGGTTATTATGAAATACAGCCACAGAGATGATGCAAGATCTTG 457
DB 344 CACAGAAAGTTTACGGGCGAGGCTACCATGACCAAGGACACGTCATCAGCAGCCTTACA 403

QY 458 AAGAGTGTGACGCTGCG 476
DB 404 TGGAGCTGACAGAGCTGAG 422

RESULT 6
US-08-017-570-3

; Sequence 3, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..373
; US-08-017-570-3

Query Match 3.3%; Score 32.2; DB 1; Length 373;

Best Local Similarity 47.3%; Pred. No. 1.3; Mismatches 106; Indels 0; Gaps 0;

QY 270 CTACCTGCTTCAAGTCTCCAGGATCAATGTGACAGATTCTTCAAGAACAGGGGCCA 329
DB 54 CAAAGATGCTCCTGACAGAGCTTGTGCTTCAACATTAAGACTATATGCACTGGGTGAA 113
QY 330 TCTGTCCCTGAGACTCATGAGACAGGTAATCTCTCTGTACTGGAAGATGTCACCCC 389
DB 114 GCAGAGGCGCTGAACAGGGCGTGGAGTGGATGGATGGATGGATGGATGGATGGATG 173
QY 390 TCAGGATACCCAGAGATTCACATGCGGGTATTATGATACAGCCACAGAGTTAGTCAA 449
DB 174 TGAATATGCCCCGAGAGTTCAGAGGCAAGCCACTATGACTACAGACACATCCTCCAAAC 233
QY 450 GATCTTGAAGAGGTGTCAGGCTG 474
DB 234 AGCTTACTGACAGCTCAGCAGCCTG 258


```

: Patent No. 580803
: GENERAL INFORMATION:
: APPLICANT: GOURLIE, BRIAN B
: APPLICANT: RIXON, MARK W
: APPLICANT: MEZES, PETER S
: APPLICANT: KAPLAN, DONALD A
: APPLICANT: SCHLOM, JEFFREY
: TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
: TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Duane C. Ulmer
: STREET: P.O. Box 1967
: CITY: Midland
: STATE: MI
: COUNTRY: US
: ZIP: 48641-1967
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/471,426
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/017,570
: FILING DATE: 16-FEB-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: ULMER, DUANE C
: REGISTRATION NUMBER: 34,941
: REFERENCE/DOCKET NUMBER: C-38,777
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (517) 636-8104
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 373 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..373
: US-08-471-426-5

Query Match 3.3%; Score 32.2; DB 1; Length 373;
Local Similarity 47.3%; Pred. No. 1.3; Mismatches 108; Indels 0; Gaps 0
hes 97; Conservative 0;

QY 270 CTACCTGCCCTTCAAGTCTCCAGGATCAATGTGACAGTTCCTCAAGACAGGGGCCA 329
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 54 CAAAGTATGTCCTGCACAGCTGTGCTTCAACATTTAAAGACTCTATATACCTAGGCTGAA 113
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
QY 330 TCTGACCTGTGACCTCATGAAGCAGGTATCTCTCTGTACCTGAAGAATGTCAACCCC 389
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 114 GCAGAGCGCTGAACAGGGCCCTGATTCGATTTGATGATTCCTCGAAGATGGTATAC 173
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
QY 390 TCAGATATCCACAGAGATTACATGCGCGGGTATTTATGAATACAGCCACAGATTAGTCAA 449
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 174 TGAATATCCCGCAGAGTTTCAGGCGCAAGGCCACTATGACTACAGACACATCTCCAACAC 233
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
QY 450 GATCTTGAAGAGGTGTGACGCTG 474
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 234 AGCTTACCTGCAGCTCAGCAGCCTG 258
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

RESULT 10
PCT-US94-01709-3
: Sequence 3, Application PC/TUS9401709
GENERAL INFORMATION:
APPLICANT: THE DOW CHEMICAL COMPANY

```

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? APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
? TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
? TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
? NUMBER OF SEQUENCES: 24
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Duane C. Ulmer
? STREET: P.O. Box 1967
? CITY: Midland
? STATE: MI
? COUNTRY: US
? ZIP: 48641-1967
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT-US94/01709
? FILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: ULMER, DUANE C
? REGISTRATION NUMBER: 34,941
? REFERENCE/DOCKET NUMBER: 38,777-F
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (517) 636-8104
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 373 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? ORIGINAL SOURCE:
? ORGANISM: Mus muscaris
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..373
PCT-US94-01709-3
?
Query Match 3.3%; Score 32.2; DB 5; Length 373;
Best Local Similarity 47.3%; Pred.No.1.3;
Matches 97; Conservative 0; Mismatches 108; Indels 0; Gaps 0
OY 270 CTACCTGCGCTTTCAGCTCCAGGCATCAATGTGGACACTTCTCTACAATAACAGGGGCCA 329
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 54 CAAGATGTCCTGCACAGCTTGCTGCTTCAACATTAAAGACTCATATATCCTGCGTGA 113
OY 330 TCTGTCCCTGAGCTCCATGAMGACAGGGTTAACTTCTCTGTACTGTAAGAATGTACCCC 389
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 114 GCAGAGGCGCTGAAGCAGGGCGCTGGATGTGATGGATGTGATCCGAGAAATGGTATAC 173
OY 390 TCAGATATCCCGACGAGTTTCACATGCGCGGGTATTATGAATACAGCCACGAGTTACTCAA 449
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 174 TGAATATCCCCCGAAGTTTCACAGGCGCACGACTATGACTACAGACACATCTCCAACAC 233
OY 450 GATCTTGAAGAGCGTGTACAGGCTG 474
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 234 AGCTTACTGCAGCTCAGCAGCCTG 238
?
RESULT 11
? PCT-US94-01709-5
? Sequence 5, Application PC/TUS9401709
? GENERAL INFORMATION:
? APPLICANT: THE DOW CHEMICAL COMPANY
? APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
? TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
? TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
? NUMBER OF SEQUENCES: 24
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Duane C. Ulmer
? STREET: P.O. Box 1967
```

CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01709
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 38,777-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..373
PCT-US94-01709-5

Query Match 3.3%; Score 32.2; DB 5; Length 373;
Best Local Similarity 47.3%; Pred. No. 1.3;
Matches 97; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 270 CTACCGCCCTTACAGTCTCCAGGAGATGTCAGAGTCTTACAGAGAGGGGCCA 329
DB 54 CAGAGATGCTCTGACAGCTTCTGCTTCAACATTAAAGACTATATGACATGGGGAA 113
QY 330 TCTGTCCCTGAGACTCCAGAGGAGTACTCTCTGTACTCTGAAGATGTCACCCC 389
DB 114 GCAGAGGCTCGAAGCAGGGCTGAGATGATGATGATGATGATGATGATGATGATG 173
QY 390 TCAGGATACCCAGAGATTACATGCCGGATTATTATGATGATGATGATGATGATG 449
DB 174 TGAATATGCCCCAGAGTCCAGGCAAGGCAAGCACTATGACACAGACATCTCCAAAC 233
QY 450 GATCTGGAAGAGTGTGTCAGGCTG 474
DB 234 AGCTTACCTGACGCTCAGCAGGCTG 258

RESULT 12
US-08-188-228-47
Sequence 47, Application US/08188228
Patent No. 559725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 3048 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-188-228-47

Query Match 3.3%; Score 32.2; DB 1; Length 3048;
Best Local Similarity 48.1%; Pred. No. 3.8;
Matches 91; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 571 TACCCAGAGCCCAACCTGATTGATCACAACAGGACATAGCCTAATAGACAGCGCT 630
DB 2052 TACCTGAGGCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2111
QY 631 CTCCAGATATACCTGCTACTGACAGAGTGGGCTGATGATGATGATGATGATGATG 690
DB 2112 CTCTCCACACGCTCATCATCAAGTCAAGTGTGCTCCATGTATACACAGGGGACTGC 2171
QY 691 AGGCTCCCTTGACATCTGCTGGGATGTTCTGTGCTGCTGCTAGAGATGTGCTCTCCAG 750
DB 2172 ACCACATTGGCCGACATGAGGAGCGCTGTGCTGCGACCGGTCATCGTGGGCAATCC 2231
QY 751 CAGACATC 759
DB 2232 ATCTGCATC 2240

RESULT 13
US-08-332-643-41
Sequence 41, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 3048 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-332-643-41
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1st Match 3.3% Score 32.2: DB 1: Length 3048:
Best Local Similarity 48.1% Pred. No. 3.8:
Matches 91: Conservative 0: Mismatches 98: Indels 0: Gaps 0:
QY 571 TACCAGAGCCCAACCTTATGTGATCAACACAGCAATAGCCTAATAGACAGGCT 630
Db 2052 TACCTGAGAGCGCGGATGTATGAGCTCCCAATCATCTGACAGACTGTGGAACCTCCC 2111
QY 631 CTGCAGATTAACACTGTCTTACTTGAACAAGTTGGCCCTGTATGATGTAAATCAGACATTAA 690
Db 2112 CTGTCAACACAGCTCATATCAAACTCAAGGTGTCCCATGTGATGACAAACGGGACTGC 2171
QY 691 AGGCTCCCTTGACATCTCGTGGGAGTGTCTGTGCTGTGAGAAATGTGGCTCTCCAC 750
Db 2172 ACGACATTTGGCGCGAGTGGCAGCGGCTGTCTGGGACACCGGTCCATCTGGCATCTCTC 2231
QY 751 CAGAACATC 759
Db 2232 ATCTGCATC 2240
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RESULT 14
US-08-332-638-47
Sequence 47, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:

```

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: NAME: No. 5646250and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31340
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-0448
: TELEFAX: (312) 474-6300
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 47:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3048 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-332-638-47

Query Match 3.3%; Score 32.2; DB 1; Length 3048;
Best Local Similarity 48.1%; Pred. No. 3.8;
Matches 91; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 571 TACCCAGAGCCCAACCTGATTTGATTCACACAGGACCAATAGCCTAATAGACAGCGCT 630
Db 2052 TACCTGGAGGCGCGGATGATGACGTCCCAATCATGCTACAGACTCTGGAAACCTCCC 2111
QY 631 CTCAGAAATAACACTGCTACTTGAACAAGTTGGCCTGTATGATGATATACAGCAATTA 690
Db 2112 CTGTCAACAGCTCATCATCAAAAGTCAAGTGTGCCATGTGATGATGACAAAGGGGACTGC 2171
QY 691 AGGCTCCCTTGACATCTCAGTGGGATGTTCTGTGCTGCGTGAAGANGTGGCTCTCCAC 750
Db 2172 ACCACCAATTTGGGCGAGTGGACGCGCTGGTGGGACCGGTGCCATCGTGCATCTTC 2231
QY 751 CAGACATC 759
Db 2232 ATCTGCATC 2240

RESULT 15
5169760-3
: PATENT NO. 5169760
: APPLICANT: WILCON, EDWARD R.
: TITLE OF INVENTION: METHOD, VECTORS AND HOST CELLS FOR
: THE CONTROL OF EXPRESSION OF HETEROLOGOUS GENES FROM LAC
: OPERATED PROMOTERS
: NUMBER OF SEQUENCES: 3
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/386,821
: FILING DATE: 27-JUL-1989
: SEQ ID NO:3:
: LENGTH: 7366
: 5169760-3

Query Match 3.3%; Score 31.4; DB 6; Length 7366;
Best Local Similarity 52.7%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 45 GCGCTGTTGAAGAAGCTCATGTTTCTAGCGGGTCTTTCTGTGCTGTGCTGTCCT 104
Db 5152 GCATCGGAGGAAAAAGCCCTGCTGCTGGCTGGCAGCATATATATGCTGACGATTAATG 5211
QY 105 GCTGCTGTGAGCAGCCCTGTGCTGCTCCTCTGCAGAGACTGAAGTCGGTGCATATG 164
Db 5212 GCTATGCTGCGCACCTCAGCGCTGGAAGTGTTATTCGTGAAGAGCGTGCATATGTTG 5271
QY 165 CAGCAATGT 173
Db 5272 AAGTACGT 5280

Search completed: November 17, 2002, 05:28:28
Job time : 62.118 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: November 17, 2002, 01:43:50 ; Search time 160.997 Seconds
(without alignments)
12085.504 Million cell updates/sec

Title: US-09-728-421D-11
Perfect score: 864
Sequence: 1 atgcgcctgycagctctctg.....tcacacacagctatgcagct 864

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2185239 seqs, 1125999159 residues

T	number of hits satisfying chosen parameters:	4370478
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Maximum DB seq length: 200000000000

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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24:	/SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT : *

Pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description
1	864	100.0	864	21	AAAG4556	DNA sequence encode
2	864	100.0	864	21	ABK87593	DNA encoding human
3	864	100.0	906	22	AAH77869	Nucleotide sequenc
4	864	100.0	953	22	AAF79921	Nucleotide sequenc
5	864	100.0	1294	21	AAAG4554	DNA sequence encod
6	864	100.0	1294	24	ABK87594	CDNA encoding huma
7	864	100.0	1453	22	AAH77870	Nucleotide sequenc
8	864	100.0	1548	22	AAU00423	Human B7-3 CDNA.
9	863.6	100.0	2114	22	ABA06726	Human CDNA SEQ ID

10	863.6	100.0	2114	22	AA58885	Human immunoglobulin
11	863.6	100.0	2751	22	AA58891	Human secreted protein
12	862.4	99.8	2616	22	ABA0634	Human cDNA SEQ ID
13	862.4	99.8	2622	22	ABA06724	Human cDNA SEQ ID
14	862.4	99.8	2622	22	AA528853	Human immunoglobulin
15	862.4	99.8	2751	22	AA528793	Human immunoglobulin
16	716	82.9	716	22	AA500474	Human BT-3 soluble
17	699.8	81.0	1831	22	AA579941	Nucleotide sequence
18	338	39.1	460	22	AA579938	cDNA clone with 5'
19	289.6	34.7	966	21	AA54555	DNA sequence encoding
20	299.6	34.7	966	24	ABK87552	cDNA encoding murine
21	299.6	34.7	2718	22	AA579919	Nucleotide sequence
22	298.4	34.5	2729	24	ABL55026	Rat cDNA isolated
23	296.4	34.3	1759	22	AA579920	Nucleotide sequence
24	277.8	32.7	1830	22	AA579942	Nucleotide sequence
25	144.6	16.7	545	21	AA543811	Mouse secreted exp
26	126.2	14.6	826	22	ABA06725	Human cDNA SEQ ID
27	126.2	14.6	826	22	AA528854	Human immunoglobulin
28	60	6.9	60	24	ABN38429	Human BT-H3 CDNA.
29	43.8	5.1	1517	22	AA500766	Human BT-H3 CDNA.
30	43.8	5.1	1517	22	AA591910	Human secreted protein
31	43.8	5.1	1998	20	AA524006	Human PRO352 nucle
32	43.8	5.1	1998	21	AA578487	Human PRO352 (UNC3
33	43.8	5.1	1998	22	AA545951	Human DNA encoding
34	43.4	5.0	3474	14	AAO39018	Sequence of pure m
35	43.4	5.0	3474	18	AA574401	Maize optimised -R.
36	43.4	5.0	3474	19	AA561611	Maize optimised DN
37	42.6	4.9	948	24	AA520546	Human B7RP-2. DNA.
38	42.2	4.9	755	22	AA160738	Human polynucleotid
39	42.2	4.9	951	24	AA520543	Human B7RP-2. DNA.
40	42.2	4.9	951	24	AA503032	Human BT-H3.1 CDNA
41	42.2	4.9	951	24	AA503033	Human BT-H3.2 CDNA
42	42.2	4.9	1463	24	ABK48096	Human dendritic cell
43	42.2	4.9	1605	24	ABK48092	DNA encoding human
44	42.2	4.9	1682	22	AA566923	Human amyloid prec
45	42.2	4.9	1683	22	AA566921	Human amyloid prec

ALIGNMENTS

RESULT 1
AAA64556
ID AAA64556 standard; DNA; 864

02-JAN-2001 (first entry)

DNA sequence encoding a human B7RP1 polypeptide

KW GNPI; CD28 related protein-1; B7Rpi, B7 related protein-1;
 KW T-lymphocyte activation; type I transmembrane protein; T cell activation
 KW T cell proliferation; T-cell mediated disorder; ss.

Homo sapiens.

Key	Location/Qualifiers
CNS	1 864

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1 40
/product= "B7Rp1"
/note= "no termination codon given"

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WO200046240-A2

10-AUG-2000

27-JAN-2000; 2000WO-US01871.

CC AIDS or AIDS-related complex, other virally or environmentally-induced
CC conditions, and certain congenital immune deficiencies. They may also
CC be employed to increase immune function that has been impaired by the
CC use of radiotherapy or immunosuppressive drugs such as certain
CC chemotherapeutic agents, and therefore are particularly useful when
CC given in conjunction with such drugs or radiotherapy. The hb7-h2
CC nucleic acid and polypeptide can be used to treat conditions
CC involving cellular immune responses, e.g., inflammatory conditions
CC (such as, for example, those induced by infectious agents including
CC *Mycobacterium tuberculosis* or *M. leprae*), or other pathologic
CC cell-mediated responses such as those involved in autoimmune diseases
CC (e.g. rheumatoid arthritis), multiple sclerosis, or insulin-dependent
CC diabetes mellitus).

XX Sequence 906 BP; 204 A; 257 C; 265 G; 180 T; 0 other;
90

Query Match	100.0%	Score 864; DB 22;	Length 906;
Best Local Similarity	100.0%;	Pred. No. 2,1e-221;	
Matches 864; Conservative	0;	Mismatches	0; Gaps 0

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Db	1 ATGGGCTGGGGACGTCTGTGACGTGCTCTTCTGCTCTTTAGACAGCTTGGACGTATCT	60
Qy	61 CAGGAGAAGGAAGTCAAGAGGATGTAAGGACAGGAGCTGAGCTCAGCTGGCCCT	120
Db	61 CAGGAGAAGGAAGTCAAGAGGATGTAAGGAGGAGCTGAGCTCAGCTGGCCCT	120
Qy	121 GAAGGAAGCCGTTTTGATTTAAATGATGTTTACGTATATTGGCAAAACAGTACGTGAAA	180
Db	121 GAAGGAAGCCGTTTTGATTTAAATGATGTTTACGTATATTGGCAAAACAGTACGTGAAA	180
Qy	181 ACCGTGTGACACTACCATCCACAGAAACAGCTCTTGGAAAACGTGGACAGCCGTAC	240
Db	181 ACCGTGTGACACTACCATCCACAGAAACAGCTCTTGGAAAACGTGGACAGCCGTAC	240
Qy	241 CGGAACCGAGCCGTGATGTACCGGCGCATGCTCGGGGACGCTTCCCTGGCTTG	300
Db	241 CGGAACCGAGCCGTGATGTACCGGCGCATGCTCGGGGACGCTTCCCTGGCTTG	300
Qy	301 TTCAACGTCAACCCCGACGAGACGAGCAAGATTCACTGCTGCTGTGTAGCCATTCCTG	360
Db	301 TTCAACGTCAACCCCGACGAGACGAGCAAGATTCACTGCTGCTGTGTAGCCATTCCTG	360
Qy	361 GGATTCAGAGAGTTTGTGACGTTTGAGGTTTACACTCATGTGGACAAACTTCAGCGTG	420
Db	361 GGATTCAGAGAGTTTGTGACGTTTGAGGTTTACACTCATGTGGACAAACTTCAGCGTG	420
Qy	421 CCGGTGTCAGCGCGCCCCACAGCCCCCTCCAGAGTAGCTCACCCTGATACATCC	480
Db	421 CCGGTGTCAGCGCGCCCCACAGCCCCCTCCAGAGTAGCTCACCCTGATACATCC	480
Qy	481 ATTAAGGGCTATACCCCAAGGCCAACGTGTACTGGATTAATAAAGCGACAAACAGCTGTG	540
Db	481 ATTAAGGGCTATACCCCAAGGCCAACGTGTACTGGATTAATAAAGCGACAAACAGCTGTG	540
Qy	541 GACCAAGCTCTGCAGATGACACCGTCTTCTTGAACATGCGGGGCTTGATACGTGTC	600
Db	541 GACCAAGCTCTGCAGATGACACCGTCTTCTTGAACATGCGGGGCTTGATACGTGTC	600
Qy	601 AGCGTGTGAGATCGCAGCGAGCCCCACGCTGAACATTGGCTGTGATAGAGACGTG	660
Db	601 AGCGTGTGAGATCGCAGCGAGCCCCACGCTGAACATTGGCTGTGATAGAGACGTG	660
Qy	661 CTTTCTGACAGAACTGACTGTGCGCAGCCAGACAGAAATGACATGGGAGAGAGAC	720
Db	661 CTTTCTGACAGAACTGACTGTGCGCAGCCAGACAGAAATGACATGGGAGAGAGAC	720
Qy	721 AAGATCAAGAGATCACTACGTACCGGCGAGAAAAAAGCGGGCACGCGAGCATCCTG	780
Db	721 AAGATCAAGAGATCACTACGTACCGGCGAGAAAAAAGCGGGCACCTGGAGCATCCTG	780
Qy	781 GCTCTCTGTGCGCTGTTGTGTCTGGGCGTGCGCCATAGGCTGGGTGTGACAGGACCGA	840

Dδ		781 GCTGTCGTGGTGCCTGCTTTGTGTG6TGCGAGGTGGCCATAGGCTGTGGTGTGCAAGSACC GA 840
Qγ	841 TGCTCACAACACAGCTATTGCAAGT 864 	
Dδ	841 TGCCTCACACACAGCTATTGCAAGT 864	

RESULT 4	
AAAF79921	
ID	AAAF79921 standard; DNA; 953 BP.

AA AC AAF79921;

DT 11-JUN-2001 (first entry)

DE Nucleotide sequence of a human GL50 polypeptide

GL50; antigen; antigen presenting cell; T cell proliferation; tumour;

KW acquired immune deficiency syndrome; AIDS; vaccine; ss.

... Homo sapiens

Key	Location/Qualifiers
-----	---------------------

```

230      /*tag= a
240      ET
250      ET

```

0200 / Produced by XX XX

XX
XX

FD-23-MAIN-2001.
XX
XX

21-SEP-2000; 2000MO-052089Z
XX

PR 21-SEP-1999; 9905-0155043.
XX

PA (GEM) GENETICS INST INC.
XX

Ling V, Dunussi-Joannopoulos K, Pi XY

DR WPI; 2001-244938/25.

XX
XX

PT immune response a

PS Claim 1; Fig 8; 195pp; English.

CC The present sequence encodes a human GL50 polypeptide. GL50

CC which costimulate T cell proliferation and bind to costimulatory

modulate an immune response in a subject. GL50 polypeptides are used

CC a tumour cell. Diseases that can be treated using GL50 molecules are

immune deficiency syndrome (AIDS), and viral infections. The GL50

CC to locate gene regions associated with genetic disease, in tissue
CC molecules can be used in vaccines. GSV polynucleotides can be used

CC typing, and in forensic identification of a biological sample.

Sequence 953 BP; 210 A; 211 C; 216 G; 190 T; 0 other;

Query Match	100.0%	Score 864;	DB 22;	Length 953;
PostgreSQL	100.0%	Prod NO	3 10-231.	

Matches	864;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

QY 1 ATGGGGCTGGCAGTCCCTGGACTGCTCTTCCCTCTTCAGCAGCCCTTCGAGCTGATACT 60

Db 24 ATGGGCTGGGAGTCCCTGGACTGCTCTTCCCTGCTCTTCAGCAGCCCTTCGAGCTGATACT 83

61 CAGGAGAAGGAGTCAGAGCCGATGGTAGGCAGCGACGTCGAGCTCAGCTGCCCTTGCCCT 120

Db 84 CAGGAGGAAGTACAGCATGGTAGGCAAGCCAGCTGAGCTCAGCTGCGCTTGCCCT 143
Qy 121 GAAGAACCCCTTTTGAATTAATGATGTTACGTATATTTGGCAACACAGTACGAAA 180
Db 144 GAAGAACCCCTTTTGAATTAATGATGTTACGTATATTTGGCAACACAGTACGAAA 203
Qy 181 ACCGTGGTACCTACCAATCCCAAGACAGCTCTTGGAAGAAAGTGGACAGCCCTAC 240
Db 204 ACCGTGGTACCTACCAATCCCAAGACAGCTCTTGGAAGAAAGTGGACAGCCCTAC 263
Qy 241 CGGAACCGAGCCCTGATGATACCGCGCGCATGCTGGCGGGGAGCTTCTCCCTGCGCTG 300
Db 264 CGGAACCGAGCCCTGATGATACCGCGCGCATGCTGGCGGGGAGCTTCTCCCTGCGCTG 323
Qy 301 TTCAACGTACACCCCAAGAGAGAGAAAGTTTCACTGCTGATGTTGAGCCAAATCCCTG 360
Db 324 TTCAACGTACACCCCAAGAGAGAGAAAGTTTCACTGCTGATGTTGAGCCAAATCCCTG 383
Qy 361 GGATTCCAGAGGTTTGGAGGTTGAGTTACACTGATGTCAGCAAACTTACGCTG 420
Db 384 GGATTCCAGAGGTTTGGAGGTTGAGTTACACTGATGTCAGCAAACTTACGCTG 443
Qy 421 CCCGTGTCAGCGCCGCCCAAGCCCTCCAGAGTACGCTACCTTACAGTATAC 480
Db 444 CCCGTGTCAGCGCCGCCCAAGCCCTCCAGAGTACGCTACCTTACAGTATAC 503
Qy 481 ATTAACGGCTACCCCAAGAGAGAGAAAGTTTCACTGCTGATGTTGAGCCAAATCCCTG 540
Db 504 ATTAACGGCTACCCCAAGAGAGAGAAAGTTTCACTGCTGATGTTGAGCCAAATCCCTG 563
Qy 541 GACGAGGCTGTCAGAAATGACACGCTTCTTGAACATGGGGGCTTGTATGACGTGTC 600
Db 564 GACGAGGCTGTCAGAAATGACACGCTTCTTGAACATGGGGGCTTGTATGACGTGTC 623
Qy 601 AGCGTGTAGAGATGCGAGCGAGCCCGAGCGTGAACATTTGGCTGCTCATAGAGAACGTG 660
Db 624 AGCGTGTAGAGATGCGAGCGAGCCCGAGCGTGAACATTTGGCTGCTCATAGAGAACGTG 683
Qy 661 CTTCGTAGAGAACTGACGTGTCGAGGAGCAAGCAAGAAATGATCGGAGAGAGAC 720
Db 684 CTTCGTAGAGAACTGACGTGTCGAGGAGCAAGCAAGAAATGATCGGAGAGAGAC 743
Qy 721 AAGATCAGAGAAATCAGTACAGCGGAGAGAAACCGCGCACAGTGGAGCATCTG 780
Db 744 AAGATCAGAGAAATCAGTACAGCGGAGAGAAACCGCGCACAGTGGAGCATCTG 803
Qy 781 GCTGTCTGTGCTGCTGTTGTGTGTGTGCGGTGGCCATAGGCTGGTGTGCAAGGACCGA 840
Db 804 GCTGTCTGTGCTGCTGTTGTGTGTGTGCGGTGGCCATAGGCTGGTGTGCAAGGACCGA 863
Qy 841 TGCCTCCACACAGCTATGCAAGT 864
Db 864 TGCCTCCACACAGCTATGCAAGT 887

RESULT 5
ID AAA64557 standard; DNA: 1294 Bp.
XX AAA64557;
AC
XX
XX 02-JAN-2001 (first entry)
XX
XX
XX DNA sequence encoding a human B7RP1 polypeptide.
XX
XX CRP1: CD28 related protein-1; B7RP1: B7 related protein-1;
XX T-lymphocyte activation; type I transmembrane protein; T cell activation;
XX T cell proliferation; T-cell mediated disorder; ss.
OS Homo sapiens.
XX
XX
FH key Location/Qualifiers

FT 5'UTR 1..199
FT /tag- a
FT CDS 200..1108
FT /tag- b
FT /product= "B7RP1"
FT sig-peptide 200..247
FT /tag- c
FT mat.peptide 248..1105
FT /tag- d
PN MO200046240-A2.
XX
XX 10-AUG-2000.
XX
XX 27-JAN-2000; 2000WO-US01871.
PF
XX
XX 03-FEB-1999; 99US-0244448.
PR 08-MAR-1999; 99US-0264527.
XX
XX (AMGE-) AMGEN INC.
XX yoshinaga SK;
XX
XX MPI: 2000-543476/49.
DR P-PSDB; AAB08729.
XX
XX Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
XX in the treatment, prevention and diagnosis of T cell mediated disorders
XX
XX Claim 2; Fig 12A; 174pp; English.
XX
XX The present sequence encodes a B7RP1 (B7 related protein-1)
XX polypeptide. The specification also describes a CRP1 (CD28 related
XX protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
XX activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
XX predicted to be a type I transmembrane protein. The nucleic acids are
XX useful for regulating T cell activation or proliferation in an animal.
XX The polypeptides are useful for treating, preventing ameliorating or
XX diagnosing a T-cell mediated disorder in an animal. They can also be
XX used to identify test molecules that bind to the polypeptides.
SQ Sequence 1294 Bp; 262 A; 400 C; 392 G; 240 T; 0 other:
Query Match 100.0%; Score 864; DB 21; Length 1294;
Best Local Similarity 100.0%; Pred. No. 2,4e-221;
Matches 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCGGCTGGGAGAGTCTGAGTCTGCTCTGCTCTTACAGACGCTTGAGCTGATCT 60
Db 200 ATGCGGCTGGGAGAGTCTGAGTCTGCTCTGCTCTTACAGACGCTTGAGCTGATCT 259
Qy 61 CAGGAGAAAGAGTACAGAGATGATGAGGAGAGAGAGTGGAGCTGAGCTGGCCCT 120
Db 260 CAGGAGAAAGAGTACAGAGATGATGAGGAGAGAGAGTGGAGCTGAGCTGGCCCT 319
Qy 121 GAAGGAAGCCGTTTGAATTAATGATGTTTACGTATATTTGCAAAACAGTGAAGTGA 180
Db 320 GAAGGAAGCCGTTTGAATTAATGATGTTTACGTATATTTGCAAAACAGTGAAGTGA 379
Qy 181 ACCGTGGTACCTACCAATCCCAAGACAGCTCTTGGAAGAAAGTGGACAGCCGCTAC 240
Db 380 ACCGTGGTACCTACCAATCCCAAGACAGCTCTTGGAAGAAAGTGGACAGCCGCTAC 439
Qy 241 CGGAACCGAGCCCTGATGATGACCGCGCATGCTGGCGGGGAGCTTCTCCCTGCGCTTG 300
Db 360 CGGAACCGAGCCCTGATGATGACCGCGCATGCTGGCGGGGAGCTTCTCCCTGCGCTTG 499
Qy 440 CGGAACCGAGCCCTGATGATGACCGCGCATGCTGGCGGGGAGCTTCTCCCTGCGCTTG 499
Db 301 TTCAACGTACACCCCAAGAGAGAGAAAGTTTCACTGCTGATGTTGAGCCAAATCCCTG 360
Qy 500 TTCAACGTACACCCCAAGAGAGAGAAAGTTTCACTGCTGATGTTGAGCCAAATCCCTG 559
Db 361 GGATTCCAGAGGTTTGGAGGTTGAGTTACACTGATGTCAGCAAACTTACGCTG 420

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DB      560 GGATTCGAGGAGCTTTGAGCGTTGAGTACATGATGGCAGCAACTTCAGCGTG 619
QY      421 CCCGTCGTCAGCGCCGCCACAGCCCCCTCCAGATGAGCTACCTTCACGTGTATCC 480
DB      620 CCCGTCGTCAGCGCCGCCACAGCCCCCTCCAGATGAGCTACCTTCACGTGTATCC 679
QY      481 ATAAAGGCTACCCAGGCGCCCAAGCTGTACTGATCAATTAAGAGGACAGCGCTGCTG 540
DB      680 ATAAAGGCTACCCAGGCGCCCAAGCTGTACTGATCAATTAAGAGGACAGCGCTGCTG 739
QY      541 GACGAGGCTCTGACAGATGACACCGCTCTTGAACATGCGGGGCTTGTATGACGTGTC 600
DB      740 GACGAGGCTCTGACAGATGACACCGCTCTTGAACATGCGGGGCTTGTATGACGTGTC 799
QY      601 ACCGTGCTAGAGATGCGACGAGACCCCGACGCTGACATGCGTGGCGCATAGAAACGTG 660
DB      800 ACCGTGCTAGAGATGCGACGAGACCCCGACGCTGACATGCGTGGCGCATAGAAACGTG 859
QY      661 CTCTGTCACAGAACCTGACTGTGCGACGACAGAGAAATGACATCGAGAGAGAGAC 720
DB      860 CTCTGTCACAGAACCTGACTGTGCGACGACAGAGAAATGACATCGAGAGAGAGAC 919
QY      721 AAGATCACAGAGAAATCCACTGATCAGTACGCGGCGGAGAAAACCGCGGACGTGAGATCTG 780
DB      920 AAGATCACAGAGAAATCCACTGATCAGTACGCGGCGGAGAAAACCGCGGACGTGAGATCTG 979
QY      781 GCGTGCCTGTCGCTGCTGTGGGTCGTGGGCGGCGGATGAGGCTGCTGACAGAGACCGA 840
DB      980 GCGTGCCTGTCGCTGCTGTGGGTCGTGGGCGGCGGATGAGGCTGCTGACAGAGACCGA 1039
QY      841 TGCCTCCAAACACAGCTATGACAGGT 864
DB      1040 TGCCTCCAAACACAGCTATGACAGGT 1063

RESULT 6
ABK87594
ID      ABK87594 standard; cDNA; 1294 BP.
XX
AC      ABK87594;
XX
DT      07-OCT-2002 (first entry)
XX
DE      cDNA encoding human B7 related protein-1 (B7RP1) #2.
XX
KW      CD28 related protein-1; CRP1; T-lymphocyte costimulatory protein;
       1gE-mediated disorder; allergy; sinus inflammation; immune disease;
       graft survival; immune activation; asthma; cancer gene immunotherapy;
       adenocarcinoma; prostate disease; leukemia; sarcoma; melanoma;
       viral infection; Hepatitis A virus; autoimmune disorder; psoriasis;
       rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
       diabetes; immunethrombocytopenic purpura; toxic shock syndrome;
       bone marrow; organ transplantation; inflammatory bowel disease;
       allogeneic transplantation; blood transfusion; graft vs. host disease; human;
       gene; ss.
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      CDS 200..1108
FT      /tag= a
FT      /product= "B7RP1"
FT      /note= "B7 related protein-1"
XX
PN      WO200244364-A2.
XX
PD      06-JUN-2002.
XX
PF      28-NOV-2001; 2001WO-US44859.
XX

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PR      28-NOV-2000; 2000US-0728420.
XX
XX      (AMGE-) AMGEN INC.
PA      (AMGE-) AMGEN CANADA INC.
XX
XX      Yoshinaga SK, Mak TW, Shahinian A, Bladt AT, Senaldi G;
DR      WPI; 2002-547698/58.
XX      P-PSDB; AAU99789.
XX
PT      Novel isolated T-lymphocyte costimulatory polypeptide, such as CD28
       related protein-1 or B7 related protein-1, useful for treating,
       preventing or ameliorating a T-cell mediated disorder in an animal
       Claim 2: Fig 12A; 197pp; English.
XX

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The invention describes an isolated T-lymphocyte costimulatory polypeptide (I), such as CD28 related protein-1 (CRP1) or B7 related protein-1 (B7RP1), and orthologues, allelic variants or alternatively sliced variants of these sequences. (I) is useful for treating, preventing, ameliorating or diagnosing a T-cell mediated disorder or a susceptibility to a T-cell mediated disorder in an animal. (I) is useful for identifying a test molecule which binds to (I) by contacting (I) with a test molecule, and determining the extent of binding of (I) to the test molecule. The method further comprises determining the activity of (I) when bound to the compound. An anti-(I) antibody is useful for suppressing an immune response in an animal, for decreasing 1gE production in an animal or for treating an 1gE-mediated disorder such as asthma, allergies, hypersensitivity and sinus inflammation. (I) and anti-(I) antibodies are useful for treating immune disease, graft survival, immune activation, T-cell dependent B-cell mediated disease, cancer gene immunotherapy (for e.g. leukemias, sarcomas, melanomas, adenocarcinomas, prostate tumours, lung carcinomas, colon carcinomas and other tumours), viral infection (e.g. by Hepatitis A virus), autoimmune disorders (such as rheumatoid arthritis, psoriasis, multiple sclerosis, diabetes, systemic lupus erythematosus and immunethrombocytopenic purpura), toxic shock syndrome, bone marrow and organ transplantation, inflammatory bowel disease, allogeneic transplantation, and for regulating the interaction of B7RP1 or CRP1. This sequence encodes the human B7 related protein-1 (B7RP1) a novel protein of the T-cell costimulatory pathway.

Sequence 1294 BP; 262 A; 400 C; 392 G; 240 T; 0 other;

Query Match 100.0%; Score 864; DB 24; Length 1294;
 Best Local Similarity 100.0%; Pred. No. 2.4e-221;
 Matches 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 ATGCGGCTGGGAGCGCTGAGCTGCTCCGCTCTTCAGCAGCGCTTGAGCTGATCT 60
DB      200 ATGCGGCTGGGAGCTGAGCTGCTCTTCGCTCTTCAGCAGCGCTTGAGCTGATCT 259
QY      61 CAGGAGAGAAAGTACAGAGCGATGTAGCAGGAGCGTGAAGTCAAGCTGCGCTTGCCCT 120
DB      260 CAGGAGAGAAAGTACAGAGCGATGTAGCAGGAGCGTGAAGTCAAGCTGCGCTTGCCCT 319
QY      121 GAAGGAAGCCGTTTATTTAAATGATGTTTACGTATTTGGCAACCGTAGTGGAAA 180
DB      320 GAAGGAAGCCGTTTATTTAAATGATGTTTACGTATTTGGCAACCGTAGTGGAAA 379
QY      181 ACCGTGCTGACCTACACATCCACAGACAGCTCTTGGAAAACGTGGACAGCGCTAC 240
DB      380 ACCGTGCTGACCTACACATCCACAGACAGCTCTTGGAAAACGTGGACAGCGCTAC 439
QY      241 CCGAACCAGCCCTGATGTACACGCGCGCATGCTCGGGGCGACTTCTCCCTGCGCTTG 300
DB      440 CCGAACCAGCCCTGATGTACACGCGCGCATGCTCGGGGCGACTTCTCCCTGCGCTTG 499
QY      301 TTCACGTACCCCGCAGAGCAGAGCAAGTTTCACTGCTGGTGTGGCAATCCGCG 360
DB      500 TTCACGTACCCCGCAGAGCAGAGCAAGTTTCACTGCTGGTGTGGCAATCCGCG 559

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QY 361,GGATCCAGAGGTTTGTAGCGTTACACTGATGTCGACGAACTTACGCTG 420
DB 560 GGATTCAGAGGAGTTTGTAGCGTTACACTGATGTCGACGAACTTACGCTG 619
QY 421 CCCGTCGACGCGCCCGACAGCCCTCCAGAGTAGGTCACCTTACGTTACATCC 480
DB 620 CCCGTCGACGCGCCCGACAGCCCTCCAGAGTAGGTCACCTTACGTTACATCC 679
QY 481 ATAAAGGCTACCCCGACGCGCCAGTCACTGATCAATAGACGACACAGCCTGCTG 540
DB 680 ATAAAGGCTACCCCGACGCGCCAGTCACTGATCAATAGACGACACAGCCTGCTG 739
QY 541 GACGAGCTCTGCAGAAATGACACCGTCTCTTGAACATGCGGGGCTGTATGAGCTGTC 600
DB 740 GACGAGCTCTGCAGAAATGACACCGTCTCTTGAACATGCGGGGCTGTATGAGCTGTC 799
QY 601 AGCGTGTGAGGATGCGACGAGCCCGACGCGTGAACATTTGGCTCTGATGAGAACGTG 660
DB 800 AGCGTGTGAGGATGCGACGAGCCCGACGCGTGAACATTTGGCTCTGATGAGAACGTG 859
QY 661 CTCTGACGAGAACTGACTGTGCGACGCCAGACAGGAAATGACATCGAGAGAGAC 720
DB 860 CTCTGACGAGAACTGACTGTGCGACGCCAGACAGGAAATGACATCGAGAGAGAC 919
QY 721 AAGATCACAGAAATCCAGTCACTGACGCGGAGAAAAAGCGGCGAGTGAAGCATCTG 780
DB 920 AAGATCACAGAAATCCAGTCACTGACGCGGAGAAAAAGCGGCGAGTGAAGCATCTG 979
QY 781 GCTGTCTGTGCTGCTTGTGTGTCGTGCGGTCGTCATAGGCTGGTGTGCGAGGACGA 840
DB 980 GCTGTCTGTGCTGCTTGTGTGTCGTGCGGTCGTCATAGGCTGGTGTGCGAGGACGA 1039
QY 841 TGCCTCCACACACACTTATGCAAGT 864
DB 1040 TGCCTCCACACACACTTATGCAAGT 1063

RESULT 7
AAH77870
ID AAH77870 standard; cDNA; 1453 BP.
AC AAH77870;
XX
XX 13-NOV-2001 (first entry)
XX
DE Nucleotide sequence of a human hb7-H2 polypeptide.
XX
XX hb7-H2; T cell stimulator; immunosuppression; cancer; AIDS;
XX congenital immune deficiency; cellular immune response;
XX inflammatory condition; autoimmune disease; rheumatoid arthritis;
XX multiple sclerosis; insulin-dependent diabetes mellitus; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FT 51..959 /*tag= a
XX FT /*product= "hb7-H2"
XX FT 51..113
XX FT sig_peptide /*tag= b
XX
XX MO200164704-A1.
XX
XX PD 07-SEP-2001.
XX
XX PF 02-MAR-2001; 2001MO-US06769.
XX
XX PR 02-MAR-2000; 2000US-0186519.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
XX PI Chen L;
XX
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DR WPI; 2001-514837/56.
DR P-PSDB; AAG67292.
XX
PT An isolated DNA encoding a hb7-H2 polypeptide, useful for treating
PT cancer, AIDS, or autoimmune diseases (e.g. rheumatoid arthritis,
PT multiple sclerosis or insulin-dependent diabetes mellitus) -
XX
XX Example 2; Fig 2A; 50bp; English.
XX
XX The present sequence encodes a human polypeptide, designated hb7-H2. The
XX hb7-H2 polypeptide co-stimulates T cells. The hb7-H2 proteins and its
XX variants are generally useful as immune response-stimulating
XX therapeutics. For example, the polypeptides can be used for treatment
XX of disease conditions characterized by immunosuppression, e.g., cancer,
XX AIDS or AIDS-related complex, other virally or environmentally-induced
XX conditions, and certain congenital immune deficiencies. They may also
XX be employed to increase immune function that has been impaired by the
XX use of radiotherapy or immunosuppressive drugs such as certain
XX chemotherapeutic agents, and therefore are particularly useful when
XX given in conjunction with such drugs or radiotherapy. The hb7-H2
XX nucleic acid and polypeptide can be used to treat conditions
XX involving cellular immune responses, e.g., inflammatory conditions
XX (such as, for example, those induced by infectious agents including
XX Mycobacterium tuberculosis or M. leprae), or other pathologic
XX cell-mediated responses such as those involved in autoimmune diseases
XX (e.g. rheumatoid arthritis), multiple sclerosis, or insulin-dependent
XX diabetes mellitus).
XX
SQ Sequence 1453 BP; 306 A; 428 C; 441 G; 278 T; 0 other;
Query Match 100.0%; Score 864; DB 22; Length 1453;
Best Local Similarity 100.0%; Pred. No. 2,5e-221;
Matches 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGGCTGGGACAGTCTCTGACAGTCTCTCTGCTTTCAGACGCTTCGAGCTGATAC 60
DB 51 ATGGGGCTGGGACAGTCTCTGACAGTCTCTCTGCTTTCAGACGCTTCGAGCTGATAC 110
QY 61 CAGGAGAAAGAGTCAAGGAGTGTAGGACGACGAGTGTGAGCTCAGCTCGCTGGCCCT 120
DB 111 CAGGAGAAAGAGTCAAGGAGTGTAGGACGACGAGTGTGAGCTCAGCTCGCTGGCCCT 170
QY 121 GAAGGAAGCCGTTTGAATTAATGATGTTTACGTATATTGGCAACCACTGAGTGA 180
DB 171 GAAGGAAGCCGTTTGAATTAATGATGTTTACGTATATTGGCAACCACTGAGTGA 230
QY 181 ACCGTGTGACTACCAATCCACAGAACAGCTCTTGGAAAAAGGAGAGCGGCTAC 240
DB 231 ACCGTGTGACTACCAATCCACAGAACAGCTCTTGGAAAAAGGAGAGCGGCTAC 290
QY 241 CGGAACCGAGCCCTGATGTACCGGCGGCGATGCTGCGGGGCGACTTCTCCGCGTTG 300
DB 291 CGGAACCGAGCCCTGATGTACCGGCGGCGATGCTGCGGGGCGACTTCTCCGCGTTG 350
QY 301 TTCAAGGTACCCCGACGAGAGAGAAATTCACGCTGCTGTGTGAGCAATCCCTG 360
DB 351 TTCAAGGTACCCCGACGAGAGAGAAATTCACGCTGCTGTGTGAGCAATCCCTG 410
QY 361 GGATTCAGAGGTTTGTAGCGTTGAGGTTACACTGATGTGCGAGAACTTACAGCGTG 420
DB 411 GGATTCAGAGGTTTGTAGCGTTGAGGTTACACTGATGTGCGAGAACTTACAGCGTG 470
QY 421 CCCGTGTACGCGCCCGACAGCCCTCCAGAGTAGAGTCACTTACAGTGTATATCC 480
DB 471 CCCGTGTACGCGCCCGACAGCCCTCCAGAGTAGAGTCACTTACAGTGTATATCC 530
QY 481 ATAAAGGCTACCCCGACGCGCCAGTCACTGATCAATAGACGACAACTGCTGCTG 540
DB 531 ATAAAGGCTACCCCGACGCGCCAGTCACTGATCAATAGACGACAACTGCTGCTG 590
QY 541 GACGAGCTCTGCAGAAATGACACCGTCTTGAACATGCGGGGCTGTATGAGCTGTC 600
DB 591 GACGAGCTCTGCAGAAATGACACCGTCTTGAACATGCGGGGCTGTATGAGCTGTC 650
```

QY 601 AGCGTGTGAGATGCGACGACGACCCCGAGCGTGAACATTGGCTGCTCATAGAGAACGTG 660
CC |||||||
CC 651 AGCGTGTGAGATGCGACGACGACCCCGAGCGTGAACATTGGCTGCTCATAGAGAACGTG 710
CC |||||||
QY 661 CTCTGTGACGAGAACCTGACTGTGCGACGACGACGAGAAATGACATCGAGAGAGAGAC 720
CC |||||||
Db 711 CTCTGTGACGAGAACCTGACTGTGCGACGACGACGAGAAATGACATCGAGAGAGAGAC 770
CC |||||||
QY 721 AAGATCACAAGAAATCCAGTACGACGACGAGAGAAACCGGCGACGTGAGAGATCTCTG 780
CC |||||||
Db 771 AAGATCACAAGAAATCCAGTACGACGACGAGAGAAACCGGCGACGTGAGAGATCTCTG 830
CC |||||||
QY 781 GCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
CC |||||||
Db 831 GCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 890
CC |||||||
QY 841 TGCCTCCACACAGACTATGACAGGT 864
CC |||||||
891 TGCCTCCACACAGACTATGACAGGT 914
CC |||||||
RESULT 8
AAS00423 standard; cDNA; 1548 BP.
XX AAS00423:
AC AAS00423:
XX 11-MAY-2001 (first entry)
XX Human B7-3 cDNA.
XX Human: B7-3; inducible co-stimulator; ICOS: TU-D: KIA0653; CD28;
KW T-cell; ICOS mediated activity; IL-10 production; TH2 activity;
KW Helicobacter pylori induced peptic ulcer; Crohn's disease;
KW multiple sclerosis; type I diabetes mellitus; graft rejection;
KW helminth infection; allergic disease; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1548
FT /tag- a
FT /partial
FT /product= "B7-3"
FT /note= "this sequence does not contain a stop codon"
XX
XX WO200112658-A2.
XX
XX 22-FEB-2001.
XX
XX 10-AUG-2000; 2000MO-GEH03079.
XX
XX 11-AUG-1999; 99US-0148402.
XX (ISIS-) ISIS INNOVATIONS LTD.
XX
XX Davis S:
PI
XX
XX WPI; 2001-226547/23.
XX P-PSDB; AAU00422.
XX
XX
XX New B7-3 polypeptides useful for modulating inducible co-stimulator
PT protein and for treating ulcers, Crohn's disease, multiple sclerosis,
PT diabetes mellitus, infections and allergic diseases
XX
XX Claim 35; Page 67; 77pp; English.
XX
XX The present sequence encodes for a novel human B7-3 protein which acts
CC as a ligand for inducible co-stimulator (ICOS) protein. The B7-3 protein
CC previously referred to as TU-D or KIA0653 was considered by the 2
CC groups as being incomplete. The present inventor has determined the
CC sequence to be complete and renamed the sequence as B7-3. Also described

CC is a soluble form of B7-3 (AAU00423) which comprises the B7-3 signal
CC sequence and extracellular domain. The extracellular domain is shown to
CC bind ICOS which is related to CD28 and expressed on T-cells. B7-3
CC polypeptides or its fragments are useful for identifying a substance
CC which interacts with the polypeptide or its fragment. B7-3 polypeptides,
CC fragments, tetramer, an agent with an ability to affect B7-3 activity or
CC a specific binding member are useful for modulating an ICOS-mediated
CC activity of T-cells by modulating IL-10 production and TH2 activity, and
CC for manufacturing a medicament for modulating an ICOS-mediated activity
CC of T-cells. B7-3 polypeptides are useful for development of diagnostic,
CC prophylactic and therapeutic agents for diseases such as Helicobacter
CC pylori induced peptic ulcers, Crohn's disease, multiple sclerosis, type
CC I diabetes mellitus, graft rejection, helminth infections, and allergic
CC diseases.
XX
SQ Sequence 1548 BP; 303 A; 472 C; 484 G; 289 T; 0 other;
Query Match 100.0%; Score 864; DB 22; Length 1548;
Best Local Similarity 100.0%; Pred. No. 2..5e-221.
Matches 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCGGCTGGGACATCTCTGACATGCTCTTCTCTTCAAGACCTTCGAGCTGATACT 60
CC |||||||
Db 1 ATGCGGCTGGGACATCTCTGACATGCTCTTCTCTTCAAGACCTTCGAGCTGATACT 60
CC |||||||
QY 61 CAGGAGAGAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
CC |||||||
Db 61 CAGGAGAGAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
CC |||||||
QY 121 GAAGGAAGCCGTTTGAATTAATGATTTAGCTATATTTGGCAAAACAGTGAATGAGAA 180
CC |||||||
Db 121 GAAGGAAGCCGTTTGAATTAATGATTTAGCTATATTTGGCAAAACAGTGAATGAGAA 180
CC |||||||
QY 181 ACCGTGTGACCTACCAATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
CC |||||||
Db 181 ACCGTGTGACCTACCAATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
CC |||||||
QY 241 CGGACCGGACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
CC |||||||
Db 241 CGGACCGGACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
CC |||||||
QY 301 TTCACGTCACCCCGACGACGAG 360
CC |||||||
Db 301 TTCACGTCACCCCGACGACGAG 360
CC |||||||
QY 361 GATTCAGAGAGTTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 420
CC |||||||
Db 361 GATTCAGAGAGTTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 420
CC |||||||
QY 421 CCGGTGTCAGCGCCCGACGACCGCCCTCCAGAGATGAGCTACCTTCAGCTGATATCC 480
CC |||||||
Db 421 CCGGTGTCAGCGCCCGACGACCGCCCTCCAGAGATGAGCTACCTTCAGCTGATATCC 480
CC |||||||
QY 481 ATAAAGCGTACCCCGACGACCGCCCTCCAGAGATGAGCTACCTTCAGCTGATATCC 540
CC |||||||
Db 481 ATAAAGCGTACCCCGACGACCGCCCTCCAGAGATGAGCTACCTTCAGCTGATATCC 540
CC |||||||
QY 541 GACGAGCTGTGAGATGACACCGCTTCTTGAACATGCGGGGCTTGTATGACGTGCTG 600
CC |||||||
Db 541 GACGAGCTGTGAGATGACACCGCTTCTTGAACATGCGGGGCTTGTATGACGTGCTG 600
CC |||||||
QY 601 AGCGTGTGAGATGCGACGACGACCCCGAGCGTGAACATTGGCTGCTCATAGAGAACGTG 660
CC |||||||
Db 601 AGCGTGTGAGATGCGACGACGACCCCGAGCGTGAACATTGGCTGCTCATAGAGAACGTG 660
CC |||||||
QY 661 CTCTGTGACGAGAACCTGACTGTGCGACGACGACGAGAAATGACATCGAGAGAGAGAC 720
CC |||||||
Db 661 CTCTGTGACGAGAACCTGACTGTGCGACGACGACGAGAAATGACATCGAGAGAGAGAC 720
CC |||||||
QY 721 AAGATCACAAGAAATCCAGTACGACGACGAGAGAAACCGGCGACGTGAGAGATCTCTG 780
CC |||||||
Db 721 AAGATCACAAGAAATCCAGTACGACGACGAGAGAAACCGGCGACGTGAGAGATCTCTG 780
CC |||||||

Oy 781 .GCTGTCCTGCTGCTGCTGCTGCGGTCATAGCTGGCTGTCAGGACCGA 840
Db 781 |GCTGTCCTGCTGCTGCTGCTGCTGCTGCGGTCATAGCTGGCTGTCAGGACCGA 840
Oy 841 TGCTCTCAACACAGCTATGACAGT 864
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RESULT 9
ABAO6726
ID ABAO6726 standard; cDNA: 2114 BP.
XX
XX ABAO6726;
XX
DT 10-JAN-2002 (first entry)
XX
DE Human cDNA SEQ ID NO: 392.
XX
XX
KX Human: gene therapy; neural disorder; immune system disorder;
KX muscular disorder; reproductive disorder; gastrointestinal disorder;
KX pulmonary disorder; cardiovascular disorder; renal disorder;
KM proliferative disorder; inflammation; ss.
XX
OS Homo sapiens.
XX
PN MO200154474-A2.
PD
XX 02-AUG-2001.
XX
PF 17-JAN-2001; 2001MO-US01349.
XX
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 24-FEB-2000; 2000US-184664P.
PR 02-MAR-2000; 2000US-186350P.
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PR 07-JUN-2000; 2000US-209467P.
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PR 26-JUL-2000; 2000US-220963P.
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PR 14-AUG-2000; 2000US-224518P.
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PR 14-AUG-2000; 2000US-225268P.
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PR 14-AUG-2000; 2000US-225447P.
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PR 23-AUG-2000; 2000US-227009P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.

PR 05-SEP-2000; 2000US-229513P.
PR 06-SEP-2000; 2000US-230437P.
PR 06-SEP-2000; 2000US-230438P.
PR 08-SEP-2000; 2000US-231242P.
PR 08-SEP-2000; 2000US-231243P.
PR 08-SEP-2000; 2000US-231244P.
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PR 08-SEP-2000; 2000US-231413P.
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PR 08-SEP-2000; 2000US-232081P.
PR 08-SEP-2000; 2000US-232081P.
PR 12-SEP-2000; 2000US-231968P.
PR 14-SEP-2000; 2000US-232387P.
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PR 14-SEP-2000; 2000US-232388P.
PR 14-SEP-2000; 2000US-232399P.
PR 14-SEP-2000; 2000US-232400P.
PR 14-SEP-2000; 2000US-232401P.
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PR 21-SEP-2000; 2000US-234223P.
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PR 25-SEP-2000; 2000US-234997P.
PR 25-SEP-2000; 2000US-234998P.
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PR 27-SEP-2000; 2000US-235834P.
PR 27-SEP-2000; 2000US-235836P.
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PR 29-SEP-2000; 2000US-236367P.
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PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 13-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239935P.
PR 13-OCT-2000; 2000US-239937P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241211P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241786P.
PR 20-OCT-2000; 2000US-241787P.
PR 20-OCT-2000; 2000US-241808P.
PR 20-OCT-2000; 2000US-241809P.
PR 20-OCT-2000; 2000US-241826P.
PR 01-NOV-2000; 2000US-244617P.
PR 08-NOV-2000; 2000US-246475P.
PR 08-NOV-2000; 2000US-246476P.
PR 08-NOV-2000; 2000US-246477P.
PR 08-NOV-2000; 2000US-246478P.
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PR 08-NOV-2000; 2000US-246532P.
PR 08-NOV-2000; 2000US-246609P.
PR 08-NOV-2000; 2000US-246610P.
PR 08-NOV-2000; 2000US-246611P.
PR 08-NOV-2000; 2000US-246613P.
PR 17-NOV-2000; 2000US-249207P.
PR 17-NOV-2000; 2000US-249208P.
PR 17-NOV-2000; 2000US-249209P.
PR 17-NOV-2000; 2000US-249210P.
PR 17-NOV-2000; 2000US-249211P.
PR 17-NOV-2000; 2000US-249212P.
PR 17-NOV-2000; 2000US-249213P.
PR 17-NOV-2000; 2000US-249214P.
PR 17-NOV-2000; 2000US-249215P.
PR 17-NOV-2000; 2000US-249216P.

CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA). The present sequence represents a human
CC secreted protein-encoding cDNA of the invention.

XX
XX Sequence 2751 BP; 593 A; 834 C; 808 G; 512 T; 4 other:

Query Match 100.0%; Score 863.6; DB 22; Length 2751;
Best Local Similarity 99.9%; Pred. No. 4e-221;
Matches 863; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGCGGCGACTCCCTGGAGCTGCTCTCTCTTTCAGACCCCTTCGAGTGACT 60
DB 218 ATGGGGGCGGCGACTCCCTGGAGCTGCTCTCTCTTTCAGACCCCTTCGAGTGACT 277
QY 61 CAGGAGAAGAGTACAGCATGTAGGCGAGCGAGCGAGCTGCGCTTGGCCT 120
D 278 CAGGAGAAGAGTACAGCATGTAGGCGAGCGAGCTGCGCTTGGCCT 337
QY 121 GAAGAAAGCCGTTTGAATTAATGATGTTACGATATTTGGCAACAGTAGTCGAAA 180
DB 338 GAAGAAAGCCGTTTGAATTAATGATGTTACGATATTTGGCAACAGTAGTCGAAA 397
QY 181 ACCGTGGAGCTACCAATCCCAAGACAGCTCCTTGGAAAAAGTGGACGCCCTAC 240
DB 398 ACCGTGGAGCTACCAATCCCAAGACAGCTCCTTGGAAAAAGTGGACGCCCTAC 457
QY 241 CGAAGCCGAGCCGTGATGTACCGCGCGCATGCTGCGGGCGCACTCTCCCTGCGCTT 300
DB 458 CGAAGCCGAGCCGTGATGTACCGCGCGCATGCTGCGGGCGCACTCTCCCTGCGCTT 517
QY 301 TTCAACTCAACCCCGAGAGAGACAGCAAGTTTCACTGCTGCTGTTGAGCCAACTCC 360
DB 518 TTCAACTCAACCCCGAGAGAGACAGCAAGTTTCACTGCTGCTGTTGAGCCAACTCC 577
QY 361 GGATTCAGAGAGTTTGTAGCGTTTACACTGATGGAGCAAACTTCAGCGTG 420
DB 578 GGATTCAGAGAGTTTGTAGCGTTTACACTGATGGAGCAAACTTCAGCGTG 637
QY 421 CCGCTGCTACGCGCCCGCCACAGCCCTCCAGAGTAGCTCACTTCACGTGTACATCC 480
DB 638 CCGCTGCTACGCGCCCGCCACAGCCCTCCAGAGTAGCTCACTTCACGTGTACATCC 697
QY 481 ATAAAGCGCTAACCCCAAGCCCAAGCTGTACTGATCAATGAAGACGCAACACCTGCTG 540
D 698 ATAAAGCGCTAACCCCAAGCCCAAGCTGTACTGATCAATGAAGACGCAACACCTGCTG 757
QY 541 GACCAGGCTGTGAGATGACACCGTCTTGAACATGGGGGCTTGTATGACGTGTC 600
DB 758 GACCAGGCTGTGAGATGACACCGTCTTGAACATGGGGGCTTGTATGACGTGTC 817
QY 601 AGCGTGTGAGATGCGACGAGCCCGCCAGCGTGAACATTGGCTGCATAGAGAAAGTG 660
DB 818 AGCGTGTGAGATGCGACGAGCCCGCCAGCGTGAACATTGGCTGCATAGAGAAAGTG 877
QY 661 CTTCGAGAGAACGTAAGTGTGAGAGCCAGCAAGAAATACATCGAGAGAGAGAC 720
DB 878 CTTCGAGAGAACGTAAGTGTGAGAGCCAGCAAGAAATACATCGAGAGAGAGAC 937
QY 721 AAGATCAAGAGAAATCACTACCGGCGAGAAAAAGCGGCGCAAGTGAACATCTTG 780
DB 938 AAGATCAAGAGAAATCACTACCGGCGAGAAAAAGCGGCGCAAGTGAACATCTTG 997
QY 781 GCTGTCTGTGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 998 GCTGTCTGTGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1057
QY 841 TGCCTCAACACAGTATGACAGT 864
DB 1058 TGCCTCAACACAGTATGACAGT 1081

RESULT 12
ID ABA06544
ID ABA06544 standard; cDNA; 2616 BP.
XX
AC ABA06544;
XX
XX 10-JAN-2002 (first entry)
DT
DE Human cDNA SEQ ID NO: 210.
XX
KW Human; gene therapy; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200154474-A2.
XX
PD 02-AUG-2001.
PF 17-JAN-2001; 2001MO-US01349.
XX
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 24-FEB-2000; 2000US-184664P.
PR 02-MAR-2000; 2000US-186350P.
PR 16-MAR-2000; 2000US-189874P.
PR 17-MAR-2000; 2000US-190076P.
PR 18-APR-2000; 2000US-198123P.
PR 19-MAY-2000; 2000US-205515P.
PR 07-JUN-2000; 2000US-209467P.
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PR 07-JUL-2000; 2000US-216880P.
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PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
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PR 23-AUG-2000; 2000US-227009P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
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PR 06-SEP-2000; 2000US-230437P.
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PR 08-SEP-2000; 2000US-231413P.

PR 08-NOV-2000; 2000US-246524P.
PR 08-NOV-2000; 2000US-246525P.
PR 08-NOV-2000; 2000US-246526P.
PR 08-NOV-2000; 2000US-246527P.
PR 08-NOV-2000; 2000US-246528P.
PR 08-NOV-2000; 2000US-246532P.
PR 08-NOV-2000; 2000US-246609P.
PR 08-NOV-2000; 2000US-246610P.
PR 08-NOV-2000; 2000US-246611P.
PR 08-NOV-2000; 2000US-246613P.
PR 17-NOV-2000; 2000US-249207P.
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PR 17-NOV-2000; 2000US-249256P.
PR 17-NOV-2000; 2000US-249297P.
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PR 17-NOV-2000; 2000US-249300P.
PR 01-DEC-2000; 2000US-250160P.
PR 01-DEC-2000; 2000US-250391P.
PR 05-DEC-2000; 2000US-251030P.
PR 05-DEC-2000; 2000US-251988P.
PR 05-DEC-2000; 2000US-256719P.
PR 06-DEC-2000; 2000US-251479P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
PR 08-DEC-2000; 2000US-251989P.
PR 08-DEC-2000; 2000US-251990P.
PR 11-DEC-2000; 2000US-254097P.
PR 05-JAN-2001; 2001US-259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM:
XX
XX P-PSDB; ABB10502.
DR
PT Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition -
XX
XX Claim 1; SEQ ID NO: 390; 859bp + Sequence Listing; English.
XX
XX The present invention provides human cDNAs, proteins and related genomic
XX DNAs. These can be used in the treatment of neutral, immune system,
XX muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
XX renal and proliferative disorders and inflammation. The present sequence
XX is a cDNA of the invention.
XX
XX Sequence 2622 BP; 567 A; 797 C; 768 G; 490 T; 0 other;
SQ
Query Match 99.8%; Score 862.4; DB 22; Length 2622;
Best Local Similarity 99.9%; Pred. No. 8.2e-221;
Matches 863; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 ATGCGGCTGGGCAATCTGAGTCTCTTCGCTTCAGCAGCCTTCAGCTGATACT 60
Db 130 ATGCGGCTGGGCAATCTGAGTCTCTTCGCTTCAGCAGCCTTCAGCTGATACT 189
OY 61 CAGGAGAAGAGTCAAGCGATGTAGGACGACGCTGAGCTCAGCTTGCCCT 120

Db 190 CAGGAGAAGAGTCAAGCGATGTAGGACGACGCTGAGCTCAGCTTGCCCT 249
OY 121 GAAGGAAGCCGTTTGGATTTAAATGATGTTTACATATTTGGCAACCACTGATCCAAA 180
Db 250 GAAAGGAAGCCGTTTGGATTTAAATGATGTTTACATATTTGGCAACCACTGATCCAAA 309
OY 181 ACCGTGGTGAACCTTACACATCCACAGACAGCTCCTTGGAAAAGCTGGACAGCCGTTAC 240
Db 310 ACCGTGGTGAACCTTACACATCCACAGACAGCTCCTTGGAAAAGCTGGACAGCCGTTAC 369
OY 241 CGGAACCGAGCCCTGATGTCAACCGCGCGGATGCTGGGGGCGACTTCTCCGCGCTTG 300
Db 370 CGGAACCGAGCCCTGATGTCAACCGCGCGGATGCTGGGGGCGACTTCTCCGCGCTTG 429
OY 301 TTCAAGCTACCCCGCAGAGACGACAGAAAGTTTACTGCTGCTGGTGTGAGCAATCCCTG 360
Db 430 TTCAAGCTACCCCGCAGAGACGACAGAAAGTTTACTGCTGCTGGTGTGAGCAATCCCTG 489
OY 361 GGATTCAGGAGGTTTGGAGGTTGAGGTTTACACTGATGAGGAGCAAACTTACGCGTG 420
Db 490 GGATTCAGGAGGTTTGGAGGTTTGGAGGTTTACACTGATGAGGAGCAAACTTACGCGTG 549
OY 421 CCCGTGCTCAGCGCCCGCCACAGCCCTCCAGAGTACGCTACACTTACAGTATAC 480
Db 550 CCCGTGCTCAGCGCCCGCCACAGCCCTCCAGAGTACGCTACACTTACAGTATAC 609
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Db 610 ATTAAGCGCTACCCCGCAGAGCAAGCTTACTGATTCATTAAGACGAGCAACAGCTCTG 669
OY 541 GACCAGGCTCTGCAGATGACACCGCTCTTGAACATGCGGGGCTGTATGACGCTGTC 600
Db 670 GACCAGGCTCTGCAGATGACACCGCTCTTGAACATGCGGGGCTGTATGACGCTGTC 729
OY 601 AGCGTGTGAGAGTGCAGCAGGACCCCGCAGCTGAACATTGAGCTGCTCATAGAACGTC 660
Db 730 AGCGTGTGAGAGTGCAGCAGGACCCCGCAGCTGAACATTGAGCTGCTCATAGAACGTC 789
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Db 790 CTTCTGACGAGAACCTGCAGCTGTGCGAGCAGCAGCAAGAAATGCAATCGGAGAGAGAC 849
OY 721 AAGATCAGAGAGATCCAGTCAGTACCGGCGAGAAAAACGCGGCACGTGAGCATCTG 780
Db 850 AAGATCAGAGAGATCCAGTCAGTACCGGCGAGAAAAACGCGGCACGTGAGCATCTG 909
OY 781 GCTGTCTGTGCTGCTGTTGTGTGTCGCGGTGCGCATAGGCTGTGTGTCAGGAGCCGA 840
Db 910 GCTGTCTGTGCTGCTGTTGTGTGTCGCGGTGCGCATAGGCTGTGTGTCAGGAGCCGA 969
OY 841 TGGCTCCACACAGCTATGACAGT 864
Db 970 TGGCTCCACACAGCTATGACAGT 993
RESULT 14
ID AAS28853 standard; cDNA; 2622 BP.
XX
XX AAS28853;
XX
XX 07-NOV-2001 (first entry)
XX
XX Human immunoglobulin encoding cDNA SEQ ID No 99.
XX
XX Immunoglobulin; primer; signal transduction pathway protein; cancer; ss;
XX antisense therapy; gene therapy; neurological disorder; renal disorder;
XX cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;
XX reproductive disorder; immune system disorder; proliferative disorder;
XX muscular disorder.
XX
XX Homo sapiens.
OS

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XX
PN      W0200155315-A2.
XX
XX      02-AUG-2001.
PD
XX
PF      17-JAN-2001: 2001W0-US01326.
XX
PR      31-JAN-2000: 2000US-0179065.
PR      04-FEB-2000: 2000US-0180628.
PR      24-FEB-2000: 2000US-0184664.
PR      02-MAR-2000: 2000US-0186350.
PR      16-MAR-2000: 2000US-0189874.
PR      17-MAR-2000: 2000US-0190076.
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PR      19-MAY-2000: 2000US-0205513.
PR      07-JUN-2000: 2000US-0209467.
PR      28-JUN-2000: 2000US-0214886.
PR      30-JUN-2000: 2000US-0215135.
PR      07-JUL-2000: 2000US-0216647.
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PR      14-JUL-2000: 2000US-0217496.
PR      26-JUL-2000: 2000US-0218290.
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PR      22-AUG-2000: 2000US-0226681.
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PR      23-AUG-2000: 2000US-0227009.
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI: 2001-457725/49.

P-PSDB; A018005.

Isolated novel immunoglobulin polypeptide for monitoring the presence and progression of diseases and for diagnosis -

Claim 1: seq ID No 39; 551bp; English.

Sequences AAS28765-AAS28877 represent cDNA molecules, which encode the immunoglobulin polypeptides of the invention, and primers for the polynucleotides. The polynucleotides and polypeptides can be used to diagnose a pathological condition or a susceptibility to a pathological condition in a subject by determining the presence or absence of a mutation in a DNA sequence or determining the presence or amount of expression of the protein. Alternatively the identification of a binding partner to a sequence allows determination of changes in protein activity. The sequences can be used as research tools for receptors or other signal transduction pathway proteins that interact with the polypeptides of the invention and can be used to treat, prevent or diagnose various types of disorders such as neurological disorders, cardiovascular disorders, gastrointestinal disorders, reproductive disorders, immune system disorders, renal disorders, muscular disorders, pulmonary disorders, proliferative disorders and cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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TITLE	Coccia, M.A.
JOURNAL	Characterization of a new human B7-related protein: B7RP-1 is the
REFERENCE	ligand to the co-stimulatory protein ICOS
AUTHORS	Unpublished
TITLE	2 (bases 1 to 909)
JOURNAL	Yoshinaga, S., K., Whoriskey, J., S., and Dai, T.
FEATURES	Submitted_16-DEC-1999 Molecular Biology Amgen Inc., One Amgen Center Drive, Thousand Oaks, CA 91320, USA Location/Qualifiers

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AUTHORS

TITLE

JOURNAL

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Patent: WO 0121796-A 5 29-MAR-2001;

FEATURES

Location/Qualifiers

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 Miyashiro, J. S., Jacobs, K. A. and Collins, M.
 Cutting edge: Identification of GL50, a novel B7-like protein that
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 J. Immunol. 164 (4), 1653-1657 (2000)
 JOURNAL MEDLINE
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 AUTHORS Ling, V.
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JOURNAL Submitted (26-OCT-1999) Immunology, Genetics Institute, 87
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 Matches 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ATGGGCTGGGCACTCCTGACACTCTCTCTCTCTTTCAGACAGCTTCGACGTGATCT 60
 DB 24 ATGGGCTGGGCACTCCTGACACTCTCTCTCTCTTTCAGACAGCTTCGACGTGATCT 83
 OY 61 CAGGAGAAGAGTACAGAGGATGTAGCAGCAGCAGTGAAGTACAGCTCGCTTGCCT 120
 DB 84 CAGGAGAAGAGTACAGAGGATGTAGCAGCAGCAGTGAAGTACAGCTCGCTTGCCT 143
 OY 121 GAAGGAAGCCGTTTGAATTAATGATGTTTACGTATATTTGGCAAAACAGTAGTGGAAA 180
 DB 144 GAAGGAAGCCGTTTGAATTAATGATGTTTACGTATATTTGGCAAAACAGTAGTGGAAA 203
 OY 181 ACCGTGTGACATCACATCCACAGACAGCTCCCTTTGAAAAACGTGGACAGCCGCTAC 240
 DB 204 ACCGTGTGACATCACATCCACAGACAGCTCCCTTTGAAAAACGTGGACAGCCGCTAC 263
 OY 241 CGGAACCGAGCCCTGATGTACCGGCGGATGCTGGGGGCGACTTCTCCCTGCGCTTG 300
 DB 264 CGGAACCGAGCCCTGATGTACCGGCGGATGCTGGGGGCGACTTCTCCCTGCGCTTG 323
 OY 301 TTCAAGCTACCCCGCAGAGCAGAGAAATTTCACCTGCTGTTGAGCCCAATCCCTG 360
 DB 324 TTCAAGCTACCCCGCAGAGCAGAGAAATTTCACCTGCTGTTGAGCCCAATCCCTG 383
 OY 361 GGATTCGAGAGGTTTATGAGGTTGAGGTTACACTGCTGTTGAGCAGCAACTTCACGCTG 420
 DB 384 GGATTCGAGAGGTTTATGAGGTTGAGGTTACACTGCTGTTGAGCAGCAACTTCACGCTG 443
 OY 421 CCCGTCGTACAGCCGCCCCACAGACCCCTCCAGAGTACGCTACCTTCACGTTGATATCC 480
 DB 444 CCCGTCGTACAGCCGCCCCACAGACCCCTCCAGAGTACGCTACCTTCACGTTGATATCC 503
 OY 481 ATTAAGGCTACCCAGGCCCAACGCTGATGATCAATAAGAGCAGACAGCCCTGCTG 540
 DB 504 ATTAAGGCTACCCAGGCCCAACGCTGATGATCAATAAGAGCAGACAGCCCTGCTG 563
 OY 541 GACCAAGCTGCAAGATGACACCGCTCTTTGAAACATGCGGGGCTTGTATGAGCTGTC 600
 DB 564 GACCAAGCTGCAAGATGACACCGCTCTTTGAAACATGCGGGGCTTGTATGAGCTGTC 623
 OY 601 AGCGTGTGAGAGATGCGACGAGACCCCGCAGCTGAAACATTTGCTGCTGATGAGAGAGCTG 660
 DB 624 AGCGTGTGAGAGATGCGACGAGACCCCGCAGCTGAAACATTTGCTGCTGATGAGAGAGCTG 683

OY	661	CTTCGACAGCAACCCTACTGTCCGGACGCCAGACAGAAATGACATCGAAGAGACGC	720
Dd	664	CTTTCGACAGCAAACCTACTGTCCGGACGCCAGACAGAAATGACATCGAAGAGAGAC	743
OY	721	AAGATCACAGAAATCAGTAGTACCGCGGAGAAAAAGCGGCCACGTGGAGCATCCGC	780
Dd	744	AAGATCACAGAAATCAGTAGTACCGCGGAGAAAAAGCGGCCACGTGGAGCATCCGC	803
OY	781	GCTGTCTGTGTGCTTGTTGTGCTGTGGCGGTGGCCATAGCTGGGTGTGACAGGACGA	840
Dd	804	GCTGTCTGTGTGCTTGTTGTGCTGTGGCGGTGGCCATAGCTGGGTGTGACAGGACGA	863
OY	841	TGCCCTCAACACAGCTATGCAGGT	864
Dd	864	TGCCCTCAACACAGCTATGCAGGT	887
<hr/>			
RESULT 4			
AX083950		1548 bp	DNA
SEQUENCE			Linear
DESCRIPTION			PAT 28-FEB-2001
SEQUENCE 1 from Patent WO0112658.			
AX083950			
AX083950.1 GI:13185508			
KEYWORDS			
SOURCE			
ORGANISM			
human.			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
Human lcos ligand and application thereof			
Patent: WO 0112658-A 1 22-FEB-2001;			
ISIS INNOVATION LIMITED (GB)			
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source			
1..1548			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
BASE COUNT			
303 a 472 c 484 g 289 t			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
100.0%; Score 864; DB 6; Length 1548;			
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1 ANGCGGCTGGGCACTCGGACTGCTCTTCTGCTCTTTCAGCAGCCTTGAGCTGATACT			
61 CAGGGAAGAAGTGTAGAGCGGATGGTAGGACGAGCGGTGAGCTGACGTGGCCTTGCCCT			
61 CAGGGAAGAAGTGTAGAGCGGATGGTAGGACGAGCGGTGAGCTGACGTGGCCTTGCCCT			
121 GAAGGAAGCGCTTTTGATTTAATGATGTTTACGTATATTGGCAAAACAGTAGTCGAAA			
121 GAAGGAAGCGCTTTTGATTTAATGATGTTTACGTATATTGGCAAAACAGTAGTCGAAA			
181 ACCGTGTGTACTTACCACATCCCAAGAACAGCTCTTGGAAAAAGTGGACACGGCGCTAC			
181 ACCGTGTGTACTTACCACATCCCAAGAACAGCTCTTGGAAAAAGTGGACACGGCGCTAC			
241 CGGAACCGAGCCCTATGTACACGGCGGCACTGTGCGGGGGGAGCTTCTCCCTGGCGCTTG			
241 CGGAACCGAGCCCTATGTACACGGCGGCACTGTGCGGGGGGAGCTTCTCCCTGGCGCTTG			
301 TTCACAGTCACCCCCAGAGCAGACAGAAATTTCACCTGCTGTGTGAGCCAATCCCTG			
301 TTCACAGTCACCCCCAGAGCAGACAGAAATTTCACCTGCTGTGTGAGCCAATCCCTG			
361 GGATTTCAGAGAGTTTGTAGCGTTGAGGTTTACAGCATGTGGCAGCAAACTTCAGCGTG			
361 GGATTTCAGAGAGTTTGTAGCGTTGAGGTTTACAGCATGTGGCAGCAAACTTCAGCGTG			
421 CCCGTCGTACGCCCCACAGCCCTTCCAGAGATGAGCTTACCTTTCACGTGTACATCC			

[illegible]

Db 369 CGGAAGCCGAGCCCTGATGTCACGGCGCGGATGCTGGGGGCGACCTTCTCCCTGCGCTTG 428
QY 301 TTCAACGTCACCCCCACAGGACGACAGAGTTTCTACTGCTGGTGTGGACCAATCCCTG 360
Db 429 TTCAACGTCACCCCCACAGGACGACAGAGTTTCTACTGCTGGTGTGGACCAATCCCTG 488
QY 361 GGATTCAGAGAGGTTTGTAGCGTTGAGTTACACTGCATGTGGCAGCAACTTCAGCGTG 420
Db 489 GGATTCAGAGAGGTTTGTAGCGTTGAGTTACACTGCATGTGGCAGCAACTTCAGCGTG 548
QY 421 CCCGTGTCAGCGCCCCACAGCCCTCCAGAGTACGTCACCTTCACGTGTACATCC 480
Db 549 CCCGTGTCAGCGCCCCACAGCCCTCCAGAGTACGTCACCTTCACGTGTACATCC 608
QY 481 ATAAAGGCTACCCCGACGCCCAAGGTACTGATCAATAAGACGCAACACAGCTCTCTG 540
Db 609 ATAAAGGCTACCCCGACGCCCAAGGTACTGATCAATAAGACGCAACACAGCTCTCTG 668
QY 541 GACCAAGCTCTGCAAGATGACACCGCTCTTGAACATGGCGGGCTGTATGAGAGTGTC 600
Db 669 GACCAAGCTCTGCAAGATGACACCGCTCTTGAACATGGCGGGCTGTATGAGAGTGTC 728
QY 601 AGCGTGTGAGAGTGCACAGGACCCCAAGGTGAACATTTGGCTGCTGCATAGAACCTG 660
Db 729 AGCGTGTGAGAGTGCACAGGACCCCAAGGTGAACATTTGGCTGCTGCATAGAACCTG 788
QY 661 CTCTGACAGAGAACTGACTGTGCGACGACAGACAGAAATGACATCGAGAGAGAC 720
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Db 849 AAGATCACAAGAAATCCAGTACGTACCGGCGAGAAAAACGCGGCACGTGAGCATCTG 908
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Db 909 GCGTCTGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968
QY 841 TGCCTCCACACAGCTATGCAAGT 864
Db 969 TGCCTCCACACAGCTATGCAAGT 992

RESULT 7
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LOCUS AX083952
DEFINITION Sequence 3 from Patent WO0112658.
ACCESSION AX083952
VERSION AX083952.1 GI:13185509
FEATURES
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Davis, S.
JOURNAL Human lcos ligand and application thereof
PATENT: WO 0112658-A 3 22-FEB-2001;
ISIS INNOVATION LIMITED (GB)
FEATURES
location/Qualifiers
source 1. 716
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 164 a 206 c 201 g 145 t
ORIGIN
Query Match 82.9%; Score 716; DB 6; Length 716;
Best Local Similarity 100.0%; Pred. No. 8.4e-148;
Matches 716; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGGGCTGGGCAATCCTGAGCTCTCTCTCTCTTTCAGACAGCTTCGAGCTGATACT 60

QY 61 CAGAGAGAGAAATCAGAGGATGTAGGAGGAGCGAGCTGAGCTGCGCTTGCCCT 120
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QY 121 GAAGGAAGCCGTTTGTATTAATGATCTTACGATATATGGCAACCACTGATGAGAA 180
Db 121 GAAGGAAGCCGTTTGTATTAATGATCTTACGATATATGGCAACCACTGATGAGAA 180
QY 181 ACCGTGTGACTTACCAATCCACAGACAGTCTCTTGGAAAACGTGGACACCGCTAC 240
Db 181 ACCGTGTGACTTACCAATCCACAGACAGTCTCTTGGAAAACGTGGACACCGCTAC 240
QY 241 CGGAACGAGCCCTGATGTACCGCGCGGATGCTGGGGGGGACCTTCTCGCGCTTG 300
Db 241 CGGAACGAGCCCTGATGTACCGCGCGGATGCTGGGGGGGACCTTCTCGCGCTTG 300
QY 301 TTCAACGTCACCCCCACAGGACGACAGAGTTTCTACTGCTGCTGTGAGCCAAATCCCTG 360
Db 301 TTCAACGTCACCCCCACAGGACGACAGAGTTTCTACTGCTGCTGTGAGCCAAATCCCTG 360
QY 361 GGATTCAGAGAGGTTTGTAGCGTTGAGTTACACTGCATGTGGCAGCAACTTCAGCGTG 420
Db 361 GGATTCAGAGAGGTTTGTAGCGTTGAGTTACACTGCATGTGGCAGCAACTTCAGCGTG 420
QY 421 CCCGTGTCAGCGCCCCACAGCCCTCCAGAGTACGTCACCTTCACGTGTACATCC 480
Db 421 CCCGTGTCAGCGCCCCACAGCCCTCCAGAGTACGTCACCTTCACGTGTACATCC 480
QY 481 ATAAAGGCTACCCCGACGCCCAAGGTACTGATCAATAAGACGCAACACAGCTCTGCTG 540
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Db 601 AGCGTGTGAGAGTGCACAGGACCCCAAGGTGAACATTTGGCTGCTGCATAGAACCTG 660
QY 661 CTCTGACAGAGAACTGACTGTGCGACGACAGACAGAAATGACATCGAGAGAG 716
Db 661 CTCTGACAGAGAACTGACTGTGCGACGACGACAGAAATGACATCGAGAGAG 716

RESULT 8
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LOCUS AK090492
DEFINITION Homo sapiens cDNA FLJ33173 fls, clone ADRL2002191, highly similar
to Homo sapiens transmembrane protein B7-H2 ICOS ligand mRNA.
ACCESSION AK090492
VERSION AK090492.1 GI:21748666
KEYWORDS oligo capping; fls (full insert sequence);
SOURCE Homo sapiens adrenal gland cDNA to mRNA, clone_11b.ADRGL2
clone:ADRL2002191.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Nishi, T., Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hito, Y., Saio, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
Sugano, S., Nagahara, K., Masuko, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
UNPUBLISHED
JOURNAL 2 (bases 1 to 2240)
REFERENCE Isogai, T. and Yamamoto, J.
AUTHORS Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 297-0812, Japan
(E-mail:genomice@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES
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/clone="ADRL2002191"
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/clone_lib="ADRL2"
/note="cloning vector: PME18SFL3"

BASE COUNT 462 a 707 c 663 g 408 t

ORIGIN
Query Match 53.3%; Score 460.4; DB 9; Length 2240;
Best Local Similarity 99.8%; Pred. No. 2e-91;
Matches 461; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

403 GCAGAACTTCAGGTCGCCGTGTCAGCCGCCACAGCCCTCCAGATGAGCTC 462
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201 GCTGAAACTTCAGGTCGCCGTGTCAGCCGCCACAGCCCTCCAGATGAGCTC 260
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463 ACCTTCAGGTCAGATCATTAACGGCTACCCAGCCCAAGCTGTACTGATTAAG 522
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261 ACCTTCAGGTCAGATCATTAACGGCTACCCAGCCCAAGCTGTACTGATTAAG 320
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321 ACGGACAACAGCCCTGCTGAGCAGGCTCTGAGATGACACCGCTCTTGAACATGG 380
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583 GGCCTTATGACGTCGTCAGGTCGTCAGGTCGTCAGGTCGTCAGGTCGTCAGGTC 642
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381 GGCCTTATGACGTCGTCAGGTCGTCAGGTCGTCAGGTCGTCAGGTCGTCAGGTC 440
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643 TGCATGATGAGAACGTCGTCGTCAGGTCGTCAGGTCGTCAGGTCGTCAGGTCGTC 702
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441 TGCATGATGAGAACGTCGTCGTCAGGTCGTCAGGTCGTCAGGTCGTCAGGTCGTC 500
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703 GACATCGGAGAGAGACAGATCAGAGATCAGTCACTGACGCGGAGAAAAACGCG 762
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763 GCCACGTGAGAGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 822
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561 GCCACGTGAGAGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
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823 TGGGTGTCAGGAGACCGATGCTCCACACAGCATATGACAGT 864
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621 TGGGTGTCAGGAGACCGATGCTCCACACAGCATATGACAGT 662

RESULT 9
IROEST054
LOCUS IROEST054 2706 bp mRNA linear PRI 10-MAY-2000
DEFINITION Homo sapiens EST from clone 34465, full insert.
ACCESSION AL355690
VERSION AL355690.1 GI:7799138
KEYWORDS EST - expressed sequence tag.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2706)
AUTHORS Aufiray,C., Ansoyge,W., Ballabio,A., Estivill,X., Gibson,K., Lehrach,H., Poustka,A. and Lundeberg,J.
TITLE The European IMAGE consortium for integrated Molecular analysis of

human gene transcripts
Unpublished
2 (bases 1 to 2706)
Carim,L., Estivill,X., Escarceller,M. and Sunmy,L.
JOURNAL
Direct Submission
Submitted (08-MAY-2000) Dept. Genetica Molecular, Institut de Recerca Oncologica (IRO), Hospital Duran i Reynals, Av. Gran Via s/n Km 2,7 L'Hospitalet de Llobregat, 08907 Barcelona, Catalunya, SPAIN. Tel: ++34-93-260-7775 Fax: ++34-93-260-7776 WWW site: http://www.iro.es e-mail enquiries: lsunmy@iro.es
EURO-IMAGE Consortium Contact: Aufiray C
CNRS UPR 420 - Genetique Molculaire et Biologie du Developpement IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8 94801 Villeneuve Cedex, FRANCE
Tel: ++33-1-49 58 34 98
Fax: ++33-1-49 58 35 09
e-mail: aufiray@infobio.fr
This clone is available royalty-free through IMAGE Consortium Distributors.
IMPORTANT: This represents single read sequence of this IMAGE cDNA clone as supplied from the European distribution centers.

FEATURES
source
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/db_xref="taxon:9606"
/clone="IMAGE cDNA clone 34465, full insert"
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/note="Matches EST Acc. Nos. R23544 and R4295"

BASE COUNT 591 a 803 c 804 g 508 t

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.1e-91;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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361 AGGTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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|||||
421 GTGTGAGGAGACCGATGCTCCACACAGCATATGACAGT 459

RESULT 10
AP001059
LOCUS AP001059/c 36230 bp DNA linear PRI 26-APR-2000
DEFINITION Homo sapiens genomic DNA, chromosome 21, clone:ID2811, MX1-D21S171 region, complete sequence.

REFERENCE AUTHORS	TITLE JOURNAL MEDLINE REFERENCE AUTHORS	TITLE JOURNAL MEDLINE REFERENCE AUTHORS	COMMENT	FEATURES source
1 (sites) Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A., Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K., Asakawa,S., Shintani,A., Sasaki,K., Nagamine,K., Mitsuyma,S., Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G., Hornischer,K., Barand,P., Scharfe,M., Schoen,O., Desario,A., Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S., Hennig,S., Riesselmann,L., Dagand,E., Wehmeyer,S., Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and Yaspo,M.L.	The DNA sequence of human chromosome 21 Nature 405 (6784), 311-319 (2000) 2 (bases 1 to 340000) Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A., Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K., Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyma,S., Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G., Hornischer,K., Barand,P., Scharfe,M., Schoen,O., Desario,A., Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S., Hennig,S., Riesselmann,L., Dagand,E., Wehmeyer,S., Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and Yaspo,M.L.	Submitted (10-Apr-2000) The Chromosome 21 Mapping and Sequencing Consortium: * Riken Genetic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below) On May 30, 2000 this sequence version replaced gi:7717422. The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genetic Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan, * e.mail: hattori@gscl.riken.go.jp * URL: http://hgp.gscl.riken.go.jp/ and * Institute of Molecular Biotechnology, Genome Analysis, * Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de * URL: http://genome.imb-jena.de/ and * Keio University School of Medicine, Molecular Biology, * Tokyo 160-8582, Japan, * e.mail: nehimizu@db-med.keio.ac.jp * URL: http://www.db.med.keio.ac.jp/ and * GBF, Dept. of Genome Analysis, * Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail: info.genome@gbf.de * URL: http://genome.gbf.de/ and * Max-Planck Institute for Molecular Genetics, * Inneistrasse 73, D-14195 Berlin, Germany, * e.mail: info-chr21@molgen.mpg.de * URL: http://chr21.rz-berlin.mpg.de/ A163298: Submitted (10-Apr-2000). Location/Qualifiers 1. 340000 /organism="Homo sapiens" /db_xref="taxon:9606" <1. 69557 /organism="Homo sapiens" /db_xref="taxon:9606"		source /chromosome="21" /map="21q22.3" /clone="KB218C10, 5' partial" /clone_lib="Keio BAC library" /note="Accession No. AP001054" 41536. .164174 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KB86A5" /clone_lib="Keio BAC library" /note="Accession No. AB001523" 15575. .198625 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD6B5" /clone_lib="KUD21-D Cosmid library" 192629. .229111 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD11C9" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001055" 219221. .255474 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD1G8" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001056" 255308. .259036 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD40G11" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001057" 258938. .298491 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD9G11" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001058" 287613. .323842 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD28B11" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001059" 314505. >340000 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD4G11, 3' partial" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001060" complement(359. .885) /note="LIMC" /rpt_family="LINE/L1" /rpt_type=DISPERSED

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repeat_region 1377..1423
      /note="(TG)n"
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      /rpt_type=TANDEM
repeat_region complement(2298..2574)
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      /rpt_family="SINE/Alu"
      /rpt_type=DISPERSED
repeat_region complement(2848..3105)
      /note="MLT1L"
      /rpt_family="LTR/MaLR"
      /rpt_type=DISPERSED
repeat_region complement(3586..3756)
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      /rpt_family="LINE/L1"
      /rpt_type=DISPERSED
repeat_region complement(3815..3984)
      /note="MLT1H"
      /rpt_family="LTR/MaLR"
      /rpt_type=DISPERSED
repeat_region complement(4103..4279)
      /note="MLT1H"
      /rpt_family="LTR/MaLR"
      /rpt_type=DISPERSED
repeat_region 4611..4723
      /note="MLT1J1"
      /rpt_family="LTR/MaLR"
      /rpt_type=DISPERSED
repeat_region complement(6887..7013)
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      /rpt_family="LTR/MaLR"
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repeat_region 7585..7791
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      /rpt_type=DISPERSED
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      /rpt_family="DNA/MERL_type"
      /rpt_type=DISPERSED
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      /rpt_type=DISPERSED

Query Match 41.1%; Score 355.4; DB 9; Length 340000;
      1st Local Similarity 97.1%; Pred. No. 1.9e-68;
      Matches 362; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 52 GCTGATCTCAGGAGGAAGTACAGAGCGATGCTAGCAGCGACGTCGAGCTCAGCTGC 111
      |||
Db 291842 GCAGATCTCAGGAGGAAGTACAGAGCGATGCTAGCAGCGACGTCGAGCTCAGCTGC 291783

QY 112 GCTTGCCCTGAAGAGCCGTTTGAATTAATGATGTTTACGTATATTGGCAACAGT 171
      |||
Db 291782 GCTTGCCCTGAAGAGCCGTTTGAATTAATGATGTTTACGTATATTGGCAACAGT 291723

QY 172 GAGTCGAAAACCGTGTGACTACCAATCCACAGAACAGCTCTTGGAAGAGTGAGAC 231
      |||
Db 291722 GAGTCGAAAACCGTGTGACTACCAATCCACAGAACAGCTCTTGGAAGAGTGAGAC 291663

QY 232 AGCCGCTACCGGAGCGACCTGATGTCACCGCGCATGCTCGGGGGGCACTTCTCC 291
      |||
Db 291662 AGCCGCTACCGGAGCGACCTGATGTCACCGCGCATGCTCGGGGGGCACTTCTCC 291603

QY 292 CTGGCGCTTGTTCACAGCTACCCGCCAGAGCAGAGAAATTTCACTGCTGCTTTGAGC 351
      |||
Db 291602 CTGGCGCTTGTTCACAGCTACCCGCCAGAGCAGAGAAATTTCACTGCTGCTTTGAGC 291543

QY 352 CAATCCCTGGAGATTCAGAGAGTTTGAAGCTTGAGCTTACAGCAATGTCAGCAAC 411
      |||
Db 291542 CAATCCCTGGAGATTCAGAGAGTTTGAAGCTTGAGCTTACAGCAATGTCAGCAAC 291483
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QY 412 TTCAGCGTCCCG 424
      |||
Db 291482 ACCATCGAGCGCG 291470

RESULT 13
AF216747 966 bp mRNA linear ROD 23-MAR-2000
LOCUS Mus musculus B7-related protein 1 mRNA, partial cds.
DEFINITION AF216747
ACCESSION AF216747.1 GI:7288510
VERSION AF216747.1
KEYWORDS
SOURCE
ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 966)
Yoshinaga,S.K., Whoriskey,J.S., Khare,S.D., Sarmiento,U., Guo,J.,
Horan,T., Shih,G., Zhang,M., Coccia,M.A., Kohno,T.,
Tatari-Bladt,A., Campbell,P., Chang,D., Chiu,L., Dai,T., Duncan,G.,
Elljott,G.S., Hui,A., McCabe,S.M., Scully,S., Shalklee,C.L., Van,G.,
Mak,T.W. and Senaldi,G.
T-cell co-stimulation through B7RP-1 and ICOS
Nature (2000) in press
2 (bases 1 to 966)
Yoshinaga,S.K. and Dai,T.
Submitted (16-DEC-1999) Molecular Biology, Amgen, Inc., One Amgen
Center Drive, Thousand Oaks, CA 91320, USA
FEATURES
source
1..966
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_type="lymphocyte"
/tissue_type="intestinal intra-epithelium"
1..>966
/note="B7RP-1; membrane bound ligand to ICOS; similar to
CD80 and CD86; unable to interact with CD28 and CTLA-4;
similar to Homo sapiens B7RP-1"
/codon_start=1
/product="B7-related protein 1"
/protein_id="AF216747.1"
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ANFSTPIVSTSDSNPQOERTYTCMSKNGYDEPLVYINTDNLIDTALQNNTVYL
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ELKVLVPIVLAIVAAAFVSFTIYRRTREHRSYTGPKIVQLELTDHA"

BASE COUNT 247 a 256 c 229 g 234 t
ORIGIN
Query Match 34.7%; Score 299.6; DB 10; Length 966;
      1st Local Similarity 64.8%; Pred. No. 7.1e-56;
      Matches 478; Conservative 0; Mismatches 254; Indels 6; Gaps 2;

QY 14 GTCTGAGCTGCTCTCTCTCTTTCAGACGCTTGAGCTGATACGAGAGAGAG 73
      |||
Db 89 GTCTGCTGTCTCTCTCTCTCTTTCAGACGCTTGAGCTGATACGAGAGAGAG 148

QY 74 TCAGAGCGATGTAGGAGCAGGAGTGAAGTCAAGCGCTGCTGGAAGAGCGCTT 133
      |||
Db 149 TCAGAGCGATGTAGGAGCAGGAGTGAAGTGAAGTCAAGCGCTGCTGGAAGAGCGCTT 208

QY 134 TTGATTTAAATGATGTTTACGTATATTGGAACCAAGTGAAGTGAACCGTGTGACCT 193
      |||
Db 209 TCAACTTGATGTGTCTATGCTATTTGGAACCAAGTGAAGTGAACCGTGTGACCT 268

QY 194 ACCAATCCACAGACAGACGCTCTTGAAAACGTGACAGCCGCTTACCGAACCAGGCC 253
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Db 269 ACTACTGCTTACAAAGTCTCCAGAGGATCAATGTGACAGATTCCTTACAAAGACAGGGGCC 328
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	Matches	478;	Conservative	0;	Mismatches	254;	Indels	6;	Gaps	2;
QY	14	GTGCTGAGATGCTGCTCTTCGCTCTTCAGAGAGCTTCGAGCTGATCTCAGAGGAAG	73							
Db	155	GCTTGTCGTGTTGTTCTTGCTGCTGTTGAGAGCCTCTGTCGCTCTGACAGACTGAG	214							
QY	74	TCAGACCGATGTTGAGCAGCGACGTGAGACTGAGCTGCGCTTGCCCTGAAGAACCGTT	133							
Db	215	TCGGTGCATAGGTGGGACACCAATGTGTCGCTCAGCTGCATTGACCCCAAGAGCCATT	274							
QY	134	TGTATTTAATATGATGTTTACGTAATTTGGCAAAACAGAGATCGCAAAACCGTGTGACT	193							
Db	275	TCAACTTGAGTGTGCTGTTATGTCTTTTGGCAATGAAAAACCCAGAACTTTTCGGTCAAT	334							
QY	194	ACCAATCCCAAGAGAACAACCTCTTGAAAAACGTGAGACAGCCGCTACCGAAGACGAGCC	253							
Db	335	ACTACCTGCTTACAAAGTCTCCAGGAGATCAATGTGACAGTTCTTACAAAGAACGGGCGC	394							
QY	254	TGATGTCACCGGCGGGAATGCTGCGGGGCGACTTCTCCCTGCGCTTTTCAACGTCAACC	313							
Db	395	ATCTGTCCCTGAGCTCCAGTAAGACAGGGTACTCTCTCTTACTCGAAGAAATGTCAACC	454							
QY	314	CCGAGGAGCAGAGAAGTTTCACTGCTGTGTGT---TGAGCAATCCCTGGGATTTCCAGG	370							
Db	455	CTCAGAGTATCCCAAGAGTTACATGCTCCGGGATTTATGATATACAGCCACAGATTACTCA	514							
QY	371	AGGTTTGAAGCGTTTATGAGTTACATGCAATGTGGCAGACAATTGACGGTCCGCTGTCA	430							
Db	515	AGATCTTGGAAAGGTGGTCAAGGCTGCTGTGGCAGCAAACTTAGTACACTGCTTCATCA	574							
QY	431	GGGCCCCCAGAGCCCTCTCCAG---ATGAGCTCACCTTACGCTGTACATCCATTAACG	487							
Db	575	GCACCTTGATAGATGCTCCAAACCGGGCCAGGAACGTACTTACCTGCATGTGCCAAGATG	634							
QY	488	GCTACCCCAAGGCCCAAGCTGTACTGTGATCAATTAAGACGAGACAGCCCTGCTGACGAG	547							
Db	635	GCTACCCCAAGGCCCAAGCTGTACTGTGATCAACACAGCGAACAATAGCTTAATAGACAGG	694							
QY	548	CTCTCACAATGACAGCGCTCTTGTGAACATGCGGGGCTTATAGACGTGTCAGCGTGC	607							
Db	695	CTCTCACAATGACAGCGCTCTTGTGAACATGCGGGGCTTATAGATGATATATCGACAT	754							
QY	608	TGAGATGCGACGAGACCCCAAGCTGTAACATTTGGCTGCTGATAGAGACGCTGCTTGC	667							
Db	755	TAAAGCTCCCTTGTGACATCTGCTGGGATGTTTGTGCTGGTATGAGATATATCGACAT	814							
QY	668	AGCAAGACCTCAGTGTGGGACGCGACAGACGAATGTGATCTCGGAGAGAGACAGATCA	727							
Db	815	ACCAAGATATACTAGCATTTTACCGACGACGAAGATTTTACTGGAATATACCAAGAAGCC	874							
QY	728	CAGAGAAATCCAGTCAGTA	745							
Db	875	CACAGAAACCCACACATA	892							
RESULT 15										
AF199027										
LOCUS	AF199027	2718 bp	mRNA	linear	ROD 17-FEB-2000					
DEFINITION	Mus musculus B7-1-like protein (G150)		mRNA, complete cds.							
ACCESSION	AF199027									
VERSION	AF199027.1	GI:6983941								
KEYWORDS										
SOURCE	Mus musculus.									
ORGANISM	Mus musculus									
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
ATTNORS	1 (bases 1 to 2718)									
	Ling, V., Wu, P. W., Fimerty, H. F., Bean, K. M., Spaulding, V., Fouser, L. A., Leonard, J. P., Hunter, S. E., Zollner, R., Thomas, J. L., Miyashiro, J. S., Jacobs, K. A. and Collins, M.									
	Cutting edge: identification of G150, a novel B7-1-like protein that functionally binds to ICOS receptor									
JOURNAL	J. Immunol.	164 (4)	1653-1657	(2000)						

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 205 a 290 c 278 g 187 t 2 others
ORIGIN

Query Match 96.8%; Score 836.6; DB 9; Length 962;

Best Local Similarity 99.4%; Pred. No. 3e-219;

Matches 858; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

1 ATGGCGCTGGGAGTCTCTGACTGCTCTCTGCTTTCAGCAGCCTTGAGCTGATCT 60
102 ATGGCGCTGGGAGTCTCTGACTGCTCTCTGCTTTCAGCAGCCTTGAGCTGATCT 161
61 CAGGAGAAAGAGTCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 120
162 CAGGAGAAAGAGTCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 221
121 GAAGGAAGCGCTTTGATTTAAATGATGTTACGTATTGGCAACCAAGTGGAGAA 180
222 GAAGGAAGCGCTTTGATTTAAATGATGTTACGTATTGGCAACCAAGTGGAGAA 281
181 ACCGTGGTACCTACCAATCCCAAGAAAGCTCTTGGAAAGCTGGACAGCCGCTAC 240
282 ACCGTGGTACCTACCAATCCCAAGAAAGCTCTTGGAAAGCTGGACAGCCGCTAC 341
241 CCGAAGCGAGCCTGATGTCACCGCGGGATGCTGCGGGGAGCTTCCCTGCGCTTG 300
342 CCGAAGCGAGCCTGATGTCACCGCGGGATGCTGCGGGGAGCTTCCCTGCGCTTG 401
301 TTCACGTCACCCCGCAGGAGCAGAGAGTTTCACTGCTGCTGTTGAGCCATCCCTG 360
402 TTCACGTCACCCCGCAGGAGCAGAGAGTTTCACTGCTGCTGTTGAGCCATCCCTG 461
361 GGATTCAGAGAGTTTGAAGCTTGAAGTTACCTGATGCTGCTGCTGCTGCTGCTG 420
462 GGATTCAGAGAGTTTGAAGCTTGAAGTTACCTGATGCTGCTGCTGCTGCTGCTG 521
421 CCGGTGTAGAGCGCCCGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480
522 CCGGTGTAGAGCGCCCGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 581
481 ATTAACGGCTACCCCGCAGGCGCCCAAGTGTACTGATCAATTAAGAGGACAAACAG 540
582 ATTAACGGCTACCCCGCAGGCGCCCAAGTGTACTGATCAATTAAGAGGACAAACAG 641
541 GACCAAGCTCTGAGATATACACCGCTTCTTAACATGCGGGGCTTGTATGACGTGTC 600
642 GACCAAGCTCTGAGATATACACCGCTTCTTAAACATGCGGGGCTTGTATGACGTGTC 701
601 AGCGTGTAGAGTCTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 660
702 AGCGTGTAGAGTCTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 761
661 CTTCCTGAGCAGAACTGACTGTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 720
762 CTTCCTGAGCAGAACTGACTGTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 821
721 AATATACAGAGAAATCCAGTACATCCGGGAGAAACCGCGGCGCAGCTGAGACATCTTG 780
822 AATATACAGAGAAATCCAGTACATCCGGGAGAAACCGCGGCGCAGCTGAGACATCTTG 881
781 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
882 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 940
841 TGCTTCCAAACAGATGATGACAGG 863

DB 941 TGCTTCCAAACAGATGATGACAGG 962

RESULT 2
BM923293
LOCUS
DEFINITION
AGENCOURT-6625900 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5758883
5', mRNA sequence.
1083 bp
EST 12-MAR-2002
IMAGE:5758883

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM923293
BM923293.1 GI:19373672
EST.
human.
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC http://mhc.nci.nih.gov/
1 (bases 1 to 1083)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs.rem@nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLNL2803 row: 9 column: 12
High quality sequence stop: 741.

Location/Qualifiers
1. organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5758883"
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/lab_host="DH10B"

/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-Sport6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA
source anonymous pool of 3 clones; age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs; 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH-MGC Library."

BASE COUNT 221 a 342 c 312 g 208 t

ORIGIN

Query Match 91.0%; Score 786.6; DB 14; Length 1083;

Best Local Similarity 99.5%; Pred. No. 1.9e-205;

Matches 789; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 ATGGCGCTGGGAGTCTCTGACTGCTCTCTGCTTTCAGCAGCCTTGAGCTGATCT 60
122 ATGGCGCTGGGAGTCTCTGACTGCTCTCTGCTTTCAGCAGCCTTGAGCTGATCT 181
61 CAGGAGAAAGAGTCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 120
182 CAGGAGAAAGAGTCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 241
121 GAAGGAAGCGCTTTGATTTAAATGATGTTTACGTATTGGCAACCAAGTGGAGAA 180
242 GAAGGAAGCGCTTTGATTTAAATGATGTTTACGTATTGGCAACCAAGTGGAGAA 301
181 ACCGTGGTACCTACCAATCCCAAGAAAGCTCTTGGAAAGCTGGACAGCCGCTAC 240
302 ACCGTGGTACCTACCAATCCCAAGAAAGCTCTTGGAAAGCTGGACAGCCGCTAC 361
241 CCGAAGCGAGCCTGATGTCACCGCGGGATGCTGCGGGGAGCTTCCCTGCGCTTG 300

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Db 362 CGGAACCGACCCCTGATGTCACCGGCGGATGTCGGGGGGAAGCTTCTCCGCGCTTG 421
Qy 301 TTCAACGTCACCCCGCAGAGCAGCAGCAAGTTTCACTGCTGCTGTTGAGCCAAATCCCTG 360
Db 422 TTCAACGTCACCCCGCAGAGCAGCAGCAAGTTTCACTGCTGCTGTTGAGCCAAATCCCTG 481
Qy 361 GGATTCGAGAGAGTTTGAAGCTTGAAGTTACATGCTGTCAGAGCAAACTTCAAGCTG 420
Db 482 GGATTCGAGAGAGTTTGAAGCTTGAAGTTACATGCTGTCAGAGCAAACTTCAAGCTG 541
Qy 421 CCCGTCGTCAGAGCCCGCAGAGCCCGTCAGAGTGAAGTCACTTCACTGATGATCC 480
Db 542 CCCGTCGTCAGAGCCCGCAGAGCCCGTCAGAGTGAAGTCACTTCACTGATGATCC 601
Qy 481 ATAAAGGCTACCCAGGCCCCCAAGCTGTACTGATCAATAAGAGAGCAAGAGCTGCTG 540
Db 602 ATAAAGGCTACCCAGGCCCCCAAGCTGTACTGATCAATAAGAGAGCAAGAGCTGCTG 661
Qy 541 GACCAAGCTGTGCAAGTACACGCTTCTTGAACATGGCGGCTGTATGAGCTGCTC 600
Db 662 GACCAAGCTGTGCAAGTACACGCTTCTTGAACATGGCGGCTGTATGAGCTGCTC 721
Qy 601 AGCGTGTGAGGATTCGACGAGACCCCGCAGCTGAACATTTGCTGCTGATGAGAGAGTG 660
Db 722 AGCGTGTGAGGATTCGACGAGACCCCGCAGCTGAACATTTGCTGCTGATGAGAGAGTG 781
Qy 661 CTTCGCGACGAAACCTGCTGCTGCGCAGCAGCAGCAAAATGACATGCGAGAGAGAGAC 720
Db 782 CTTCGCGACGAAACCTGCTGCTGCGCAGCAGCAGCAAAATGACATGCGAGAGAGAGAC 841
Qy 721 AAGATACAGAGAAATTCAGTACGAGGAGCAAAACGCGGCGAGCTGAGAGATCTG 780
Db 842 CAGATCAGGAGAAATTCAGTACGAGGAGCAAAACGCGGCGAGCTGAGAGATCTG 901
Qy 781 GCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 914
Db 902 GCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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LOCUS BM543561 978 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6492731 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5726681
5', mRNA sequence.
ACCESSION BM543561
VERSION BM543561.1 GI:18774056
KEYWORDS EST.
SOURCE human.
ANIM human.
REFERENCE 1 (bases 1 to 978)
AUTHORS NIH-MGC http://mgi.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM12719 row: 1 column: 18
High quality sequence stop: 708.
Location/Qualifiers
1..978
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age 27. Library is oligo-dT primed and directionally
cloned (EcorV site is destroyed upon cloning). Average
insert size 1.4 kb. Insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."
BASE COUNT 203 a 301 c 290 g 183 t 1 others
ORIGIN
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Query Match 84.0% Score 725.6; DB 13; Length 978;
Best Local Similarity 95.0%; Pred. No. 1.1e-188;
Matches 771; Conservative 0; Mismatches 39; Indels 2; Gaps 2;
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Qy 1 ATCGGCTGGGAGTCCCTGAGTCTCTTCCCTGCTCTTCCAGCAGCTTGCAGCTGATCT 60
Db 135 ATCGGCTGGGAGTCCCTGAGTCTCTTCCCTGCTCTTCCAGCAGCTTGCAGCTGATCT 194
Qy 61 CAGAGAGAGAGTCAAGAGGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 195 CAGAGAGAGAGTCAAGAGGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
Qy 121 GAAGGAGAGAGTCTTGAATGATGTTTACGTATATTGGCAAAACAGTGAAGTGA 180
Db 255 GAAGGAGAGAGTCTTGAATGATGTTTACGTATATTGGCAAAACAGTGAAGTGA 314
Qy 181 ACCGTGTGACCTACACATCCACAGAAACAGTCTCTTGAAGAGAGAGAGAGAGAGAG 240
Db 315 ACCGTGTGACCTACACATCCACAGAAACAGTCTCTTGAAGAGAGAGAGAGAGAGAG 374
Qy 241 CGGAACCGAGCCCTGATGTCACCGGCGGAGTACGCGGAGAGAGAGAGAGAGAGAGAG 300
Db 375 CGGAACCGAGCCCTGATGTCACCGGCGGAGTACGCGGAGAGAGAGAGAGAGAGAGAG 434
Qy 301 TTCAACGTCACCCCGCAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 435 TTCAACGTCACCCCGCAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 494
Qy 361 GGATTCGAGAGAGTTTGAAGCTTGAAGTTACATGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 495 GGATTCGAGAGAGTTTGAAGCTTGAAGTTACATGCTGCTGCTGCTGCTGCTGCTGCTG 554
Qy 421 CCCGTCGTCAGAGCCCGCAGAGCCCGTCAGAGTGAAGTCACTTCACTGATGATCC 480
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Qy 481 ATAAAGGCTACCCAGGCCCCCAAGCTGTACTGATCAATAAGAGAGCAAGAGCTGCTG 540
Db 615 ATAAAGGCTACCCAGGCCCCCAAGCTGTACTGATCAATAAGAGAGCAAGAGCTGCTG 674
Qy 541 GACCAAGCTGTGCAAGTACACGCTTCTTGAACATGGCGGCTGTATGAGCTGCTC 600
Db 675 GACCAAGCTGTGCAAGTACACGCTTCTTGAACATGGCGGCTGTATGAGCTGCTC 734
Qy 601 AGCGTGTGAGGATTCGACGAGACCCCGCAGCTGAACATTTGCTGCTGATGAGAGAGT 659
Db 735 AGCGTGTGAGGATTCGACGAGACCCCGCAGCTGAACATTTGCTGCTGATGAGAGAGT 794
Qy 660 GCTTCGAGAGAGAGTCAAGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
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Qy 720 CAAGATCAGAG-AGAATTCAGTACGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 778
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Qy 779 TGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 810
Db 915 TCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 946
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RESULT 4
BI488470      816 bp  mRNA  linear  EST 28-AUG-2001
LOCUS        60302097121 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191864 5',
DEFINITION   mRNA sequence.
ACCESSION    BI488470
VERSION      BI488470.1 GI:15327698
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiade; Homo.
REFERENCE    1 (bases 1 to 816)
AUTHORS      NIH-MGC http://mhc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: c9apbs-r@mail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM1479 row: m column: 17
              High quality sequence stop: 790.
              Location/Qualifiers
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                 /lab_host="DH10B"
                 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                 Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                 male brains, age range 23-27 yo. Library is oligo-dT
                 primed and directionally cloned (EcoRV site is destroyed
                 upon cloning). Average insert size 1.5 kb, insert size
                 range 1-3 kb. Library is normalized and enriched for
                 full-length clones and was constructed by C. Gruber
                 (Invitrogen). Research Genetics tracking code 019. Note:
                 this is a NIH-MGC Library."
BASE COUNT   166 a 258 c 230 g 162 t
ORIGIN
Query Match 70.3%; Score 607.4; DB 13; Length 816;
at Local Similarity 99.0%; Pred. No. 3.6e-156;
Matches 674; Conservative 0; Mismatches 1; Indels 6; Gaps 6;

QY 1 ATGGCGCTGGGCACTCTCGACCTGCTTCTTCAGCAGCCCTTCAGCGATAC 60
    |||||||
Db 134 ATGGCGCTGGGCACTCTCGACCTGCTTCTTCAGCAGCCCTTCAGCGATAC 193

QY 61 CAGGAGAAGAGTCAGAGCGATGTAGCAGCGACCTGAGCTCAGCTGGCTTGCC 120
    |||||||
Db 194 CAGGAGAAGAGTCAGAGCGATGTAGCAGCGACCTGAGCTCAGCTGGCTTGCC 253

QY 121 GAAGGAGCCCTTTGATTAAATGATGTTTACGTATATTGGCAACCACTGAGTC 180
    |||||||
Db 254 GAAGGAGCCCTTTGATTAAATGATGTTTACGTATATTGGCAACCACTGAGTC 313

QY 181 ACCGTGTGACCTACCAACATCCACAGAACGCTCTGGAAAGCGTGAGACCGCTAC 240
    |||||||
Db 314 ACCGTGTGACCTACCAACATCCACAGAACGCTCTGGAAAGCGTGAGACCGCTAC 373

QY 241 CGGAACCGAGCCCTGATGTACACCGCGGCGCATGCTGCGGGCGACTTCTCCCTG 300
    |||||||
Db 374 CGGAACCGAGCCCTGATGTACACCGCGGCGCATGCTGCGGGCGACTTCTCCCTG 433

QY 301 TTCAACGTCACCCCGAGAGCAGACAGATTTCACCTGCTGCTGTTGAGCCATCCCTG 360
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Db 434 TTCAACGTCACCCCGAGAGCAGACAGATTTCACCTGCTGCTGTTGAGCCATCCCTG 493

QY 361 GGATTCCAGAGAGGTTTGTAGCGTTGAGGTTCACATGTCGAGGAACTTACGGTG 420
    |||||||
Db 494 GGATTCCAGAGAGGTTTGTAGCGTTGAGGTTCACATGTCGAGGAACTTACGGTG 553

QY 421 CCCGTCGTCAGAGCCGCCACAGCCGCCCTCCAGATGAGCTCACCTTCACGTATCC 480
    |||||||
Db 554 CCCGTCGTCAGAGCCGCCACAGCCGCCCTCCAGATGAGCTCACCTTCACGTATCC 613

QY 481 AT-AAACGGTACCCCGACGCCCAACGCTGCTACTGATCATATAGACGGAACAA-GCCTGC 538
    |||||||
Db 614 ATAAACGGTACCCCGACGCCCAACGCTGCTACTGATCATATAGACGGAACAA-GCCTGC 673

QY 539 TGGACAGAGCTCTGAGAAATGACACCGCTCTTGAACA-TGCCGAGGCTTGATGAGTG 597
    |||||||
Db 674 TGGACAGAGCTCTGAGAAATGACACCGCTCTTGAACA-TGGCGAGGCTTGATGAGTG 733

QY 598 GTACACGTCGT-GAGATACGACGAGACCCCGACGCTG-AACATTGGCTTGATAGAGA 655
    |||||||
Db 734 GTACACGTCGTGAGATACGACGAGACCCCGACGCTGAAACATGGGCTGTGATAGAGA 793

QY 656 ACG-TGCTTTCGACGACAGAC 675
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Db 794 ACGTTGCTTTCGACGACAGAC 814

RESULT 5
AM377686      486 bp  mRNA  linear  EST 04-FEB-2000
LOCUS        PM2-CT0238-290999-001-f03 CT0238 Homo sapiens cDNA, mRNA sequence.
DEFINITION   AM377686
ACCESSION    AM377686
VERSION      AM377686.1 GI:6882349
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiade; Homo.
REFERENCE    1 (bases 1 to 486)
AUTHORS      HCGP http://www.ludwig.org.br/ORESTES.
TITLE        The FAPESP/LICR Human Cancer Genome Project
JOURNAL      Unpublished (1999)
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?fl=PM2&lt2=PM2-CT0238-
              290999-001-f03&lt3=1999-09-29&lt4=1)
              Seq primer: puc 18 forward
              High quality sequence start: 2
              High quality sequence stop: 485.
              Location/Qualifiers
                1..486
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /clone_lib="CT0238"
                 /dev_stage="Adult"
                 /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                 SmaI; A mini-library was made by cloning products derived
                 from ORESTES PCR (U.S. Letters Patent application No. 196
                 716 - Ludwig Institute for Cancer Research) profiles
                 into the puc 18 vector. Reverse transcription of tissue
                 mRNA and cDNA amplification were performed under low
                 stringency conditions."
BASE COUNT   112 a 140 c 136 g 98 t
ORIGIN
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Query Match 50.6%; Score 437.2; DB 10; Length 486;
 Best Local Similarity 97.7%; Pred. No. 2e-109; Indels 3; Gaps 3;
 Matches 475; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

263 CGGCCGCGATGCTGC-GGGCGCACTTCTCCGCGCTTGTTCAGTCACCCCGAGAC 321
 1 CGTCGCGCTGCTGGCGGCGACCTTCTCCGCGCTTGTTCAGTCACCCCGAGAC 60
 322 GAGCAGAACTTTCACCTGCTGTTGAGCCAACTCCCTGGGATTCCAGAGCTTTGAC 381
 61 GAGCAGAACTTTCACCTGCTGTTGAGCCAACTCCCTGGGATTCCAGAGCTTTGAGC 120
 382 GTTGAAGTTTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 440
 121 ATTGAAGTTTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 441 CAGCCCTTCCAGATGAGCTTACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
 181 CAGCCCTTCCAGATGAGCTTACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 501 CACGCTGTACTGATCAATTAAGACGACAGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 559
 241 CACGCTGTACTGATCAATTAAGACGACAGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 560 ACACGCTTCTTGAACATGCGGGCTTGTATGACGCTGCTGCTGCTGCTGCTGCTGCTG 619
 301 ACACGCTTCTTGAACATGCGGGCTTGTATGACGCTGCTGCTGCTGCTGCTGCTGCTG 360
 620 GAGCCCTTCCAGATGAGCTTACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 679
 361 GAGCCCTTCCAGATGAGCTTACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 680 CTGTGCGCAGCAGACAGAAATGACATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 739
 421 CTGTGCGCAGCAGACAGAAATGACATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 740 TCAGTA 745
 481 TCAGTA 486

RESULT 6 496 bp mRNA linear EST 28-APR-2000
 LOCUS AM753046
 DEFINITION PM2-CT0238-290999-001-g01 CT0238 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AM753046
 VERSION AM753046.1 GI:7667978
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 496)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brines, M.R.,
 Negal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldstein, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brumstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM2&t2=PM2-CT0238-
 290999-001-g01&t3=1999-09-29&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 8
 High quality sequence stop: 39.
 Location/Qualifiers
 1. 496
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CT0238"
 /dev_stage="Adult"
 /note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2:
 Sma1; A mini-library was made by cloning products derived
 from ORSTES PCR (U.S. Letters Patent application No. 196
 '716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions." 94 t

BASE COUNT 126 a 139 c 137 g 94 t

Query Match 50.4%; Score 435.4; DB 10; Length 496;
 Best Local Similarity 96.2%; Pred. No. 6.3e-109;
 Matches 478; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

303 CACGCTACCCCGAG 362
 1 CACGCTAACCCCGAG 59
 363 ATTCCAG 422
 60 ATTCCAG 119
 423 CGTGTGAGCGCCCGCCAGACGCCCTTCCAGATGAGCTTCACTTCACTTCACTTCACT 481
 120 CGTGTGAGCGCCCGCCAGACGCCCTTCCAGATGAGCTTCACTTCACTTCACTTCACT 179
 482 TAAACGGCTACCCCGAG 541
 180 TAAACGGCTACCCCGAG 239
 542 ACCAGGCTTGCAGAAATGACACCGCTTCTTGAACATGCGGGCTTGTATGACAGTGTCA 601
 240 AACAGGCTTGCAGAAATGACACCGCTTCTTGAACATGCGGGCTTGTATGACAGTGTCA 299
 602 GCGTGTGAGATGCGACGAG 661
 300 GCGTGTGAGATGCGACGAG 359
 662 TTCTGAGCAGAACTGATGCTGTGCGGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 721
 360 ATTGAGCAGAGAACTGATGCTGTGCGGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
 722 AGATTCAGAGAACTGATGCTGTGCGGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 420 AGATTCAGAGAACTGATGCTGTGCGGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 479
 781 GCTGTCTGTGCTGTCT 797
 480 GGTGTCTGTGCTGTCT 496

RESULT 7 448 bp mRNA linear EST 04-FEB-2000
 LOCUS AM377683
 DEFINITION PM2-CT0238-290999-001-f02 CT0238 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AM377683
 VERSION AM377683.1 GI:6882346
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 448)
 HCGP <http://www.ludwig.org.br/ORESTES>.
 AUTHORS The FAPESP/LICR Human Cancer Genome Project
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM2&t2=PM2-CT0238-290999-001-f02&t3=1999-09-29&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 5
 High quality sequence stop: 221.
 Location/Qualifiers

1. 448
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CT0238"
 /dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 128 a 115 c 119 g 86 t
 ORIGIN

Query Match 43.4%; Score 375.2; DB 10; Length 448;
 Best Local Similarity 94.2%; Pred. No. 2.3e-92;
 Matches 422; Conservative 0; Mismatches 23; Indels 3; Gaps 3;

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OY 314 CCCGAGCAGCAGCAAAATTTTCACTGCTGTTGAGCCCAATCCCTGGGANTCCAGAGG 373
Db 1 CCCAGGAGCAGCAGCAAAATTTTCACTGCTGTTGAGCCCAATCCCTGGGANTCCAGAGG 60
OY 374 TTTGAGCGTTGAGGTTTACACTGCATGTCGAGCAAACTTCAGCGTCCCTGCTCAGCG 433
Db 61 TTATGACATTGAGGTTTACACTGCATGTCGAGCAAACTTCAGCGTCCCTGCTCAGCG 120
OY 434 CCCCCCAAGCCCTCCAGAGTACGCTCACCCTTCACGTTGATCATTCATTAAGCGCTACC 493
Db 121 CCCCCCAAGCCCTCCAGAGTACGCTCACCCTTCACGTTGATCATTCATTAAGCGCTACC 180
OY 494 CCAGGCCCAAGCTGATGATCAATAG-ACGACAACAGCCGTCGGAGCAGGCTC-T 551
Db 181 CCAGGCCCAAGCTGATGATCAATAGAGAGCAACACACATGCTGGACAGGCTCTT 240
OY 552 GCAGATGACACCGCTCTTGAACATGCGGGCTTGATGACGTTGTCACCGTCTGAG 611
Db 241 GGAATATGACACCGCTCTTGAACATGCGGGCTTGATGACGTTGTCACCGTCTGAG 300
OY 612 GATC-GCAGCAGCCCGCAGCGTGAACATGCTGCTGATGAGAACCTGCTTGTGAGC 670
Db 301 GATCGGAAGGAGCCCGCAGCGTGAACATGCTGCTGATGAGAACCTGCTTGTGAGC 360
OY 671 AGAAGCTGATGTCGCGCAGCAGAGCAATGACATGAGAGAGAGACAAGATCAG 730
Db 361 ATTAAGCTGATGTCGCGTACGAGAGCAAGAAATGACATGAGAGAGAGACAAGATCAG 420
OY 731 AGAATCAGTCAGTACGCGGCGAGAAAA 758
Db 421 AGAATCAGTCAGTACGCGGCGAGAAAA 448

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RESULT 8

R23544
 LOCUS R23544 422 bp mRNA linear EST 20-APR-1995
 DEFINITION Yg34c12.11 Soares infant brain IN1B Homo sapiens cDNA clone
 IMAGE:34465 5', mRNA sequence.
 ACCESSION R23544
 VERSION R23544.1 GI:778432
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 422)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
 M., Hultman,M., Kuwaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
 Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisakis,E., Waterston
 R., Williamson,A., Woldmann,P. and Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 2783

High quality sequence stops: 364 Source: IMAGE Consortium, LINT
 This clone is available royalty-free through LINT; contact the
 IMAGE Consortium (info@image.jnl.gov) for further information.
 Insert Length: 2783 Std Error: 0.00
 Seq primer: M3RPL
 High quality sequence stop: 364.
 Location/Qualifiers

FEATURES
 source

1. 422
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 /db_xref="GDB:406812"
 /db_xref="taxon:9606"
 /clone="IMAGE:34465"
 /clone_lib="Soares Infant brain IN1B"
 /sex="female"
 /dev_stage="73 days post natal"
 /note="Organ: whole brain; Vector: latmid BA; Site_1: Not
 I; Site_2: Hind III; 1st strand cDNA was primed with a Not
 I - oligo(dT) primer [5'
 AACTGGAGAGATTGCGCGCGGAGGAGAAATTTTGTGTTTGTGTTT 3'];
 double-stranded cDNA was ligated to Hind III adaptors
 (pharmacia), digested with Not I and directionally cloned
 into the Not I and Hind III sites of the latmid BA vector.
 Library went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 100 a 122 c 121 g 78 t 1 others
 ORIGIN

Query Match 42.2%; Score 365; DB 14; Length 422;
 Best Local Similarity 100.0%; Pred. No. 1.4e-89;
 Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 407 CAAACTTCAGCGCCCGTGTGAGCGCCGCCACAGACCCCTCCAGAGTACCTACCT 466
Db 1 CAAACTTCAGCGCGCCGCTGTGAGCGCCGCCACAGACCCCTCCAGAGTACCTACCT 60
OY 467 TCACGTTATCATTAAGAGGCTACCCGAGGCCAAGGTGATGATTAATAGAGG 526
Db 61 TCACGTTATCATTAAGAGGCTACCCGAGGCCAAGGTGATGATTAATAGAGG 120
OY 527 ACAACAGCCTGCTGAGCAGGCTCTGAGATGACACACCGTCTTGAACATGCGGGCT 586
Db 121 ACAACAGCCTGCTGAGCAGGCTCTGAGATGACACACCGTCTTGAACATGCGGGCT 180
OY 587 TGTATGACGTGTCAGCGTGTGAGATTCGACAGGAGCCCGACGCTGAATATGGCTGCT 646
Db 181 TGTATGACGTGTCAGCGTGTGAGATTCGACAGGAGCCCGACGCTGAATATGGCTGCT 240

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QY 647 GCATAGAGACGCTGCTTTCGACGAGAACCTGACTGCGGACGACAGAGAAATGACA 706
|||||
Db 241 GCATAGAGACGCTGCTTTCGACGAGAACCTGACTGCGGACGACAGAGAAATGACA 300
QY 707 TCGAGAGAGAGACAAAGATCACAGAGAAATCCAGTACGTACCGCGGAGAAACGCGGCCA 766
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Db 301 TCGAGAGAGAGACAAAGATCACAGAGAAATCCAGTACGTACCGCGGAGAAACGCGGCCA 360
QY 767 CCGTG 771
|||||
Db 361 CCGTG 365

RESULT 9
BF776710 476 bp mRNA linear EST 25-APR-2001
LOCUS 287583 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BF776710
ACCESSION BF776710.1 GI:12124610
VERSION EST.
KEYWORDS COW.
SOURCE Bos taurus
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 476)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennet,
G.B., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G.,
Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mainscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAAT
BACKWARD: GTTTCACAGTCACGAGC
Plate: 92 row: J column: 22
Seq primer: ATTGAGTGCACCTATAG.
Location/Qualifiers
1..476
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/db_xref="taxon:9913"
/clone.lib="MARC 3BOV"
/tissue.type="pooled"
/lab.host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT 111 a 139 c 141 g 85 t
ORIGIN

Query Match 26.6%; Score 230; DB 12; Length 476;
Best Local Similarity 72.0%; Pred. No. 2,3e-52;
Matches 347; Conservative 0; Mismatches 120; Indels 15; Gaps 3;

QY 357 CCGGATTCGAGAGAGCTTTGAGCTGAGTACATGCAATGGCAGCAACTTACG 416
|||||
Db 4 CCTGGAAATTAATAAAAGATTGGAACTTGGGACAGGTCGCGAGCAAACTACAG 63
|||||
QY 417 CCGTCCGCTGTCAGCGCCCGACAGCCCTCCCGATGAGCTCAGCTTACGCTGAC 476
|||||

Db 64 CATTGCTGTGTGTCAGCGGCCGT-----CCAGAGACAGAGAGCTTCACCTTCAGCTGCAC 117
QY 477 ATCCATTAAGCGCTACCCAGAGCCCAACGTGATGATCAATAGACGAGACAGCCT 536
|||||
Db 118 GCTTACCAAGCGCTACCCCGGCAATATGTACTGATCAACAGACGAGACAGCCT 177
|||||
QY 537 GCTGAGCAAGCGCTTCCAGAAATGACACCGCTCTTGAACATGCGGGGCTTGATACGT 596
|||||
Db 178 GCTGAGACCGCCCTGCAAAATTAACAGGCTGTCCCTGAACGCGGGGCTGTATGATGT 237
QY 597 GGTACAGCTGCTGAGAGATGCAGCAGACCCAGCGTGAACATTGCTGCTATAGAA 656
|||||
Db 238 GGTCACTGTCTCTAGAAATGGGGGAACCCCGCATGTCAACGTGCTGCTATAGAA 297
QY 657 CGTCTTTCGACAGACACCTGACTGTGCGACGACAGAGAAATGACATGGAGAGAG 716
|||||
Db 298 TGTGCTGTACACCAACACCTGCAC---GAGCGCGACAGAGAAACGTTCACGGAGCAA 354
QY 717 AGCAGATCACAGAGAAATCCAGT-----CAGTACCGCGAGAAACGCGGCCACGTG 770
|||||
Db 355 GGACAGCATCACAGAGACCGAGTGCATGAGCCAGCCCGGAGAAACACGAGAGGTTT 414
QY 771 GAGCATCTGCGCTGTCTGTGCTGCTGCTGTGCTGCTGCGGCGTGCATGAGCTGCTG 830
|||||
Db 415 TAGCGTCTTGGCGTCTGCGCGTGTGATCGTCTGCTGCTGCGCAGCGGCTGCTG 474
QY 831 CA 832
Db 475 CA 476

RESULT 10
BI911468 771 bp mRNA linear EST 16-OCT-2001
LOCUS BI911468
DEFINITION 603063908F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5213400 5',
mRNA sequence.
ACCESSION BI911468
VERSION BI911468.1 GI:16175218
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 771)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM11535 row: O column: 01
High quality sequence start: 19
High quality sequence stop: 414.
Location/Qualifiers
1..771
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/db_xref="taxon:9606"
/clone.lib="IMAGE:5213400"
/clone.lib="NIH_MGC_118"
/tissue.type="leukocyte"
/lab.host="DH10B"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb. Insert size range
1.2-3.3 kb. Library is normalized and enriched for

Best Local Similarity 98.2%; Pred. No. 9.9e-34;

18.7%; score 161.4; DB 1/; Length 165;
98.28; Pred. No. 9.9e-34;

cdna library was prepared and sequenced in Mouse Genome

Kono, H., Fukunishi, T., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001).

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamakawa, I., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. *Genome.* 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resesgsc.riken.go.jp,
url: http://genome-gsc.riken.go.jp/
Carninci, H., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Ito,
'M., Kono, H., Ozekaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to

FEATURES

SOURCE

Query Match	15.5%;	Score 134;	DB 10;	Length 661;
Best Local Similarity	61.6%;	Pred. No. 7.5e-26;		
Matches 250; Conservative	0;	Mismatches 150;	Indels 6;	Cases 2

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Db      496  CATCTTGCCCTGGACTCCATTAAGACAGGGGGTACTTCTTTCTTGACCCGTGAAATATCACCC 553
QY      313  CCCAGAGACGACGAGAAGTTTCACTGCCTGGTGT-----TGAACCAATCCCTGGAGATTCC 367
Db      556  CTCACAGATACCCACAGGAGATTACATGCCCCGGGTATTATTAAGATTACAGCCCAAGATTAG 615
QY      368  AGGAGGTTTTTGAGCGCTTGAGTTACACTGCATGATGAGGACCAAACTT 413
Db      616  TCAAGATCTTGAAGAAGAGTGTCAGCGTGCCTGTGACACCAACTT 661

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Search completed: November 17, 2002, 05:26:42
 Job time : 1257.62 secs

Search completed: November 17, 2002, 05:26:42
Job time : 1257.62 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 17, 2002, 04:46:36 ; Search time 37.2984 Seconds

(without alignments)
8559.585 Million cell updates/sec

Title: US-09-728-421D-11

Perfect score: 864
1 atgcggctggcgacgtcctg.....tcacacacgtatgcaggt 864

Sequence: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Scored table: 328367 seqs, 184756068 residues

T number of hits satisfying chosen parameters: 656734

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	863.6	100.0	2114	10	US-09-764-853-392
2	863.6	100.0	2751	10	US-09-789-561-64
3	862.4	99.8	2616	10	US-09-764-853-210
4	862.4	99.8	2622	10	US-09-764-853-390
5	126.2	14.6	826	10	US-09-764-853-391
6	43.8	5.1	1517	10	US-09-789-561-63
7	43.8	5.1	1998	9	US-09-978-295A-136
8	43.8	5.1	1998	12	US-10-052-586-53
9	42.6	4.9	948	10	US-09-910-174A-27
10	42.6	4.9	951	10	US-09-910-174A-23
11	42.2	4.9	2097	10	US-09-875-338-8
12	42.2	4.9	3197	10	US-09-875-338-6
13	42.2	4.9	3197	10	US-09-875-338-19
14	40.2	4.7	951	10	US-09-875-338-10
15	40.2	4.7	3436	10	US-09-789-561-12
16	40	4.6	951	10	US-09-875-338-12
17	38.2	4.4	2214	10	US-09-867-694A-1
18	36	4.2	479	10	US-09-867-701-4120
19	35.8	4.1	2602	10	US-09-917-800A-1590

20	35.6	4.1	2473	12	US-10-052-586-559	Sequence 559, App
21	35.4	4.1	855	10	US-09-815-242-7681	Sequence 7681, Ap
22	35.4	4.1	1587	9	US-09-712-363-48	Sequence 48, Appl
23	35.2	4.1	2943	9	US-09-954-531-993	Sequence 993, Appl
24	35.2	4.1	2943	10	US-09-954-456-217	Sequence 217, App
25	35.2	4.1	2943	10	US-09-880-107-2316	Sequence 2316, Ap
26	34.6	4.0	3401	9	US-09-905-291A-249	Sequence 249, App
27	34.6	4.0	3401	10	US-09-909-320-249	Sequence 249, App
28	34.6	4.0	3401	10	US-09-909-088B-249	Sequence 249, App
29	34.6	4.0	4428	10	US-10-052-586-411	Sequence 411, App
30	34.6	4.0	211	10	US-09-833-381-1364	Sequence 1364, Ap
31	34.4	4.0	211	10	US-09-960-352-4718	Sequence 4718, Ap
32	34.4	4.0	999	9	US-09-925-664-46	Sequence 46, Appl
33	34.4	4.0	1060	10	US-09-791-171-13	Sequence 13, Appl
34	34.4	4.0	1882	9	US-09-954-531-178	Sequence 178, App
35	34.4	4.0	1882	9	US-09-954-531-386	Sequence 386, App
36	34.4	4.0	1882	9	US-09-954-531-594	Sequence 594, App
37	34.4	4.0	1894	10	US-09-939-483-1	Sequence 1, Appl
38	34.4	4.0	1894	10	US-09-939-483-1	Sequence 1, Appl
39	34.2	4.0	467	10	US-09-864-761-2131	Sequence 2131, Ap
40	34.2	4.0	570	10	US-09-864-761-7685	Sequence 7685, Ap
41	34.2	4.0	2126	12	US-10-052-586-495	Sequence 495, App
42	34.2	4.0	2261	10	US-09-823-356-21	Sequence 21, Appl
43	33.8	3.9	26555	9	US-09-860-670-161	Sequence 161, App
44	33.6	3.9	883	10	US-09-867-550-1905	Sequence 1905, Ap
45	33.6	3.9	3957	10	US-09-764-853-77	Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-09-764-853-392
; Sequence 392, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; PRIORITY FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 392
; LENGTH: 2114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2003)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2078)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2091)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2095)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-392
Query Match 100.0%; Score 863.6; DB 10; Length 2114;
Best Local Similarity 99.9%; Pred. No. 2.9e+240;
Matches 863; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCGGCTGGCGAGCTGCTCTTCTGCTCTTACAGACGCTTGAGCTGACT 60
DB 129 ATGCGGCTGGCGAGCTGCTCTTCTGCTCTTACAGACGCTTGAGCTGACT 188
QY 61 CAGGAGAGAGAGTACAGACGATGATGAGCAGCAGCTGAGCTGAGCTGCGCT 120
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Db 189 CAGGAGGAAGGATCGAGACCGATGGTAGGACGAGCAGTGGAGCTCGACGTCGGCTTGCCT 248
QY 121 GAGGAGAGCCGTTTGTATTTAAATGATGTTTACGTATATGGCAAAACAGTAGTCGAAA 180
Db 249 GAGGAGAGCCGTTTGTATTTAAATGATGTTTACGTATATGGCAAAACAGTAGTCGAAA 308
QY 181 ACCGTTGAGTACCTACACATCCACAGAAACAGTCTCTTGGAAAGGTGACAGCCGCTAC 240
Db 309 ACCGTTGAGTACCTACACATCCACAGAAACAGTCTCTTGGAAAGGTGACAGCCGCTAC 368
QY 241 CGGAACCGAGCCCTGATGTACCGGCGGCGATGCTGCGGGGCGACTTCTCCCTGCGCTTG 300
Db 369 CGGAACCGAGCCCTGATGTACCGGCGGCGATGCTGCGGGGCGACTTCTCCCTGCGCTTG 428
QY 301 TTCAACGTCACCCCGGAGAGCAGCAAGATTTCACCTGCTGCTGTTGAGCCAACTCCCTG 360
Db 429 TTCAACGTCACCCCGGAGAGCAGCAAGATTTCACCTGCTGCTGTTGAGCCAACTCCCTG 488
QY 361 GGATTCCAGAGGTTTGTAGCGTTGAGTTACATGTCATGTCAGCAACTTCAGCCGTG 420
Db 489 GGATTCCAGAGGTTTGTAGCGTTGAGTTACATGTCATGTCAGCAACTTCAGCCGTG 548
QY 421 CCGCTGTCAGCGCCCGCCACAGCCCTTCCAGATGAGCTCACTTCACTGTATATCC 480
Db 549 CCGCTGTCAGCGCCCGCCACAGCCCTTCCAGATGAGCTCACTTCACTGTATATCC 608
QY 481 ATAAAGGCTACCCCGAGGCCCAAGGTACTGATCTAATAAGAGGACAAAGCCGCTTG 540
Db 609 ATAAAGGCTACCCCGAGGCCCAAGGTACTGATCTAATAAGAGGACAAAGCCGCTTG 668
QY 541 GACCAAGCTCTGTCAGATGACACCGCTCTTCTGAACATGCGGGGCTTGTATACGTGTC 600
Db 669 GACCAAGCTCTGTCAGATGACACCGCTCTTCTGAACATGCGGGGCTTGTATACGTGTC 728
QY 601 ACCGTGCTGAGATGCGACGAGACCCCGACGCTGATGCTGCTGCTAGAGAACGTG 660
Db 729 ACCGTGCTGAGATGCGACGAGACCCCGACGCTGATGCTGCTGCTAGAGAACGTG 788
QY 661 CTTTGCACAGAACTGACTGCTGCGGACGCCAGAGAAATGACATCGGAGAGAGAC 720
Db 789 CTTTGCACAGAACTGACTGCTGCGGACGCCAGAGAAATGACATCGGAGAGAGAC 848
QY 721 AAGATCACAGAAATCAGTACGATCCGGCGAGAAAAACCGGCGCACGTGAGACATCTG 780
Db 849 AAGATCACAGAAATCAGTACGATCCGGCGAGAAAAACCGGCGCACGTGAGACATCTG 908
QY 781 GCTGTCTGTGCTGCTGTGTGTCGTGGGCGGTGGCCATAGGCTGGGTGTGCAAGGACGA 840
Db 909 GCTGTCTGTGCTGCTGTGTGTCGTGGGCGGTGGCCATAGGCTGGGTGTGCAAGGACGA 968
QY 841 TGCCTCCAAACACAGCTATGCAAGT 864
Db 969 TGCCTCCAAACACAGCTATGCAAGT 992

RESULT 2
US-09-789-561-64
; Sequence 64, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; FILE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: P2043p1
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: *PatentIn Ver. 2.0
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; SEQ ID NO 64
; LENGTH: 2751
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-789-561-64

Query Match          100.0%; Score 863.6; DB 10; Length 2751;
Best Local Similarity 99.9%; Pred. No. 3.3e-240;
Matches 863; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGGCTGGGAGTCCTGAGTCTGCTTCTGCTCTTCTGCTCTGACAGCCCTTGACCTATCT 60
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QY 61 CAGGAGAAAGAGTACAGACCGATGGTAGGACAGGAGTGGAGCTCAGCTGCGCTTGCCCT 120
Db 278 CAGGAGAAAGAGTACAGACCGATGGTAGGACAGGAGTGGAGCTCAGCTGCGCTTGCCCT 337
QY 121 GAGGAGAGCCGTTTGTATTTAAATGATGTTTACGTATATGGCAAAACAGTAGTCGAAA 180
Db 338 GAGGAGAGCCGTTTGTATTTAAATGATGTTTACGTATATGGCAAAACAGTAGTCGAAA 397
QY 181 ACCGTGCTGACTACCAATCCCAAGAAACAGTCTCTTGGAAAAGGTGACAGCCGCTAC 240
Db 398 ACCGTGCTGACTACCAATCCCAAGAAACAGTCTCTTGGAAAAGGTGACAGCCGCTAC 457
QY 241 CGGAACCGAGCCCTGATGTACCGGCGGCGATGCTGCGGGGCGACTTCTCCCTGCGCTTG 300
Db 458 CGGAACCGAGCCCTGATGTACCGGCGGCGATGCTGCGGGGCGACTTCTCCCTGCGCTTG 517
QY 301 TTCAACGTCACCCCGGAGAGCAGCAAGATTTCACCTGCTGCTGTTGAGCCAACTCCCTG 360
Db 518 TTCAACGTCACCCCGGAGAGCAGCAAGATTTCACCTGCTGCTGTTGAGCCAACTCCCTG 577
QY 361 GGATTCCAGAGGTTTGTAGCGTTGAGTTACATGTCATGTCAGCAACTTCAGCCGTG 420
Db 578 GGATTCCAGAGGTTTGTAGCGTTGAGTTACATGTCATGTCAGCAACTTCAGCCGTG 637
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Db 638 CCGCTGTCAGCGCCCGCCACAGCCCTTCCAGATGAGCTCACTTCACTGCTGATATCC 697
QY 481 ATAAAGGCTACCCCGAGGCCCAAGCTGTACTGATCTAATAAGAGGACAAAGCCGCTTG 540
Db 698 ATAAAGGCTACCCCGAGGCCCAAGCTGTACTGATCTAATAAGAGGACAAAGCCGCTTG 757
QY 541 GACCAAGCTCTGTCAGATGACACCGCTCTTCTGAACATGCGGGGCTTGTATACGTGTC 600
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QY 601 ACCGTGCTGAGATGCGACGAGACCCCGACGCTGTAACATTGGCTGCTGCTATAGAGAACTG 660
Db 818 ACCGTGCTGAGATGCGACGAGACCCCGACGCTGTAACATTGGCTGCTGCTATAGAGAACTG 877
QY 661 CTTTGCACAGAACTGACTGCTGCGGACGCCAGACGAAATGACATCGGAGAGAGAC 720
Db 878 CTTTGCACAGAACTGACTGCTGCGGACGCCAGACGAAATGACATCGGAGAGAGAC 937
QY 721 AAGATCACAGAAATCAGTACGATCCGGCGAGAAAAACCGGCGCACGTGAGACATCTG 780
Db 938 AAGATCACAGAAATCAGTACGATCCGGCGAGAAAAACCGGCGCACGTGAGACATCTG 997
QY 781 GCTGTCTGTGCTGCTGTGTGTCGTGGGCGGTGGCCATAGGCTGGGTGTGCAAGGACGA 840
Db 998 GCTGTCTGTGCTGCTGTGTGTCGTGGGCGGTGGCCATAGGCTGGGTGTGCAAGGACGA 1057
QY 841 TGCCTCCAAACACAGCTATGCAAGT 864
Db 1058 TGCCTCCAAACACAGCTATGCAAGT 1081

RESULT 3
US-09-764-853-210
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; Sequence 210, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 210
; LENGTH: 2616
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-210

Query Match 99.8%; Score 862.4; DB 10; Length 2616;
Best Local Similarity 99.9%; Pred. No. 7,1e-240;

Matches 863; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 CAGGAGAAGAAAGTCAGAGCGATGTAGGCAAGCGAGCGTGGAGCTGAGCTTGGCCT 120
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Db 184 CAGGAGAAGAAAGTCAGAGCGATGTAGGCAAGCGAGCGTGGAGCTGAGCTTGGCCT 243
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QY 121 GAAGGAAGCCGTTTGAATTAATGATGTTACGTATATTGGCAACAGTGAAGTGA 180
    |||||||
Db 244 GAAGGAAGCCGTTTGAATTAATGATGTTACGTATATTGGCAACAGTGAAGTGA 303
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QY 181 ACCGTGTGACTATCCATCCCAAGACAGCTCTTGGAAAAAGTGGACAGCCGTAC 240
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QY 241 CGGAACCGAGCCCTGATGTACCGCGCGCATGCTGGGGGCGACTTCCTCGCGCTTG 300
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Db 364 CGGAACCGAGCCCTGATGTACCGCGCGCATGCTGGGGGCGACTTCCTCGCGCTTG 423
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QY 301 TTCACGTCACCCCGCCAGAGAGAGAGAGAGTTCACCTGCTGTGTGAGCCAACTCCCTG 360
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Db 424 TTCACGTCACCCCGCCAGAGAGAGAGAGAGTTCACCTGCTGTGTGAGCCAACTCCCTG 483
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QY 361 GGATTCAGAGAGTTTGAAGCTTGAAGTTACACTGATGTGGAGCAAACTTCAAGCTG 420
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Db 484 GGATTCAGAGAGTTTGAAGCTTGAAGTTACACTGATGTGGAGCAAACTTCAAGCTG 543
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QY 421 CCGGTGTCAGCGCCCGCCAGAGCCCTCCAGAGATGAGTCACTTCAAGTGAATCC 480
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Db 544 CCGGTGTCAGCGCCCGCCAGAGCCCTCCAGAGATGAGTCACTTCAAGTGAATCC 603
    |||||||

QY 481 ATAAAGGCTACCCCGAGGCCAAAGTGTACTGATCAATTAAGAGAGCAACAGCTGCTG 540
    |||||||
Db 604 ATAAAGGCTACCCCGAGGCCAAAGTGTACTGATCAATTAAGAGAGCAACAGCTGCTG 663
    |||||||

QY 541 GACAGAGCTTGAAGATGACACCGCTTCTTGAACATGGGGGCTTGTATGACGTGCTC 600
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Db 664 GACAGAGCTTGAAGATGACACCGCTTCTTGAACATGGGGGCTTGTATGACGTGCTC 723
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QY 601 AGCGTGTAGATGCGACGAGACCCCGAGCGTGAACATTGGCTGTGATAGAGAGCTG 660
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Db 724 AGCGTGTAGATGCGACGAGACCCCGAGCGTGAACATTGGCTGTGATAGAGAGCTG 783
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QY 661 CTTCCTGAGAGAACTGACTGTGCGAGCGACAGACAGAAATGACATCGAGAGAGAGAC 720
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Db 784 CTTCCTGAGAGAACTGACTGTGCGAGCGACAGACAGAAATGACATCGAGAGAGAGAC 843
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QY 721 AAGATCAGAGAGAACTGAGTACGCGGAGAAAAAGCGGGCCAGCGTGGAGCATCTCG 780
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Db 964 TGCCTCCACAGACGCTATGACAGT 987
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RESULT 4

US-09-764-853-390
; Sequence 390, Application US/09764853
; Patent No. US20020090672A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1206

; CURRENT APPLICATION NUMBER: US/09/764,853
; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 390
; LENGTH: 2622

; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-764-853-390

Query Match 99.8%; Score 862.4; DB 10; Length 2622;
Best Local Similarity 99.9%; Pred. No. 7,1e-240;

Matches 863; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 130 ATGCGGCTGGGCACTCTGAGCTCTTCTCTCTTTCAGACGCTTTCAGCTGATACT 189
    |||||||

QY 61 CAGGAGAAGAAAGTCAGAGCGATGTAGGCAAGCGAGCGTGGAGCTGAGCTTGGCCT 120
    |||||||
Db 190 CAGGAGAAGAAAGTCAGAGCGATGTAGGCAAGCGAGCGTGGAGCTGAGCTTGGCCT 249
    |||||||

QY 121 GAAGGAAGCCGTTTGAATTAATGATGTTACGTATATTGGCAACAGTGAAGTGA 180
    |||||||
Db 250 GAAGGAAGCCGTTTGAATTAATGATGTTACGTATATTGGCAACAGTGAAGTGA 309
    |||||||

QY 181 ACCGTGTGACTATCCATCCCAAGACAGCTCTTGGAAAAAGTGGACAGCCGTAC 240
    |||||||
Db 310 ACCGTGTGACTATCCATCCCAAGACAGCTCTTGGAAAAAGTGGACAGCCGTAC 369
    |||||||

QY 241 CGGAACCGAGCCCTGATGTACCGCGCGCATGCTGGGGGCGACTTCCTCGCGCTTG 300
    |||||||
Db 370 CGGAACCGAGCCCTGATGTACCGCGCGCATGCTGGGGGCGACTTCCTCGCGCTTG 429
    |||||||

QY 301 TTCACGTCACCCCGAGAGAGAGAGAGTTCACCTGCTGTGTGAGCCAACTCCCTG 360
    |||||||
Db 430 TTCACGTCACCCCGAGAGAGAGAGAGTTCACCTGCTGTGTGAGCCAACTCCCTG 489
    |||||||

QY 361 GGATTCAGAGAGTTTGAAGCTTGAAGTTACACTGATGTGGAGCAAACTTCAAGCTG 420
    |||||||
Db 490 GGATTCAGAGAGTTTGAAGCTTGAAGTTACACTGATGTGGAGCAAACTTCAAGCTG 549
    |||||||

QY 421 CCGGTGTCAGCGCCCGCCAGAGCCCTCCAGAGATGAGTCACTTCAAGTGAATCC 480
    |||||||
Db 550 CCGGTGTCAGCGCCCGCCAGAGCCCTCCAGAGATGAGTCACTTCAAGTGAATCC 609
    |||||||

QY 481 ATAAAGGCTACCCCGAGGCCAAAGTGTACTGATCAATTAAGAGAGCAACAGCTGCTG 540
    |||||||
Db 610 ATAAAGGCTACCCCGAGGCCAAAGTGTACTGATCAATTAAGAGAGCAACAGCTGCTG 669
    |||||||

QY 541 GACAGAGCTTGAAGATGACACCGCTTCTTGAACATGGGGGCTTGTATGACGTGCTC 600
    |||||||
Db 670 GACAGAGCTTGAAGATGACACCGCTTCTTGAACATGGGGGCTTGTATGACGTGCTC 729
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QY 601 AGCGTGTAGATGCGACGAGACCCCGAGCGTGAACATTGGCTGTGATAGAGAGCTG 660
    |||||||
```


APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
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2 PRIOR APPLICATION NUMBER: 60/084414
3 PRIOR FILING DATE: 1998-05-06
4 PRIOR APPLICATION NUMBER: 60/084441
5 PRIOR FILING DATE: 1998-05-06
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16 PRIOR APPLICATION NUMBER: 60/084627
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18 PRIOR APPLICATION NUMBER: 60/084643
19 PRIOR FILING DATE: 1998-05-07
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21 PRIOR FILING DATE: 1998-05-13
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27 PRIOR FILING DATE: 1998-05-15
28 PRIOR APPLICATION NUMBER: 60/085700
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36 PRIOR APPLICATION NUMBER: 60/085573
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38 PRIOR APPLICATION NUMBER: 60/085704
39 PRIOR FILING DATE: 1998-05-15
40 PRIOR APPLICATION NUMBER: 60/085697

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	Query Match	Similarity	5.1%;	Score 43.8;	DB 9;	Length 1998;
	Local Similarity	47.0%;	Pred. No. 0.0033;			
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OY	224	ACGTGAGACGCCGCTACCGGAACCGAGCCCTGATGCACCGGCCGGCATGCTCGGGGCGC	283			
Db	402	ACCAAGGACGCGCTATGCAACCCACAGCGCCCTCTTCGCCGACCTGCTGCACAGGCA	461			
Db	284	ACTTCTCCCTCGCGCTTTTCAACGTCACCCCCCAGSAGACGAGAAGTTTCACTGCTCTGG	343			
OY	462	ACGCATCCCTTAGGCTGACGCGCGTGCGCTGTGGGAGACAGGAGGACGTTCCACTCTGTTGG	521			
Db	344	TGTTWAGCCCAATCCCTGGGATTCCAGAGAGTTTTAGCCTTGAGCTTACATGCAATGTGG	403			
Db	522	TGAGATCCGGGATTTTCGGCACGCGCTGCCGTGAGCCTGAGAGTGGCGCTCCCTA-----	576			
OY	404	CAGCAACTTACAGCTGCGCCGCTGTCAGCGCCGCCAACAGCCCTTCCACGATGAGCTCA	463			
Db	577	-CTCBAAGCCCGCCAGCTGAGCCCTCTGGAGGCCCAACAAGGAACTTGCGGCGAGGACACGCTGA	635			
OY	464	CCTTACGCTGATCATTCATAAAGCGCTTAACCCAGGCGCCCAACGTCGACTGATCAATTAAGA	523			
Db	636	CCATACAGTGCCTCCACGCTACCAAGGGCTTACCTTGAAGGCTGAGGTGTTCTTGTGCAAGATGGGC	695			
OY	534	CGGACAAACGCCCTGCTGGAGACCAAGGCTCTGCAATATGACACCGCTCTTCTTGAACATCGGG	583			
Db	696	AGGGTGTGCCCTTGACTGGAACGTHAGACACGTGCGAGATGGCC-----AACGACAGG	749			
OY	584	GCTTGTATGACGTGTCACGCTGCTGAGAGATGACACAGAACCCCCACGCTGAACATTTGGCT	643			
Db	750	GCTTGTGTGATGTGACAGCGCTCGTCGGGAGTGCTGTGGTGTGCGAATGGCACTTACAGCT	809			

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0y      644   GCTGATAGACACGTGGTTCGTGCAGCAGA 674
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Db      810   GCCTGCTCCGCAACCCTGCTGCACGACGA 840

RESULT 8
US-10-052-586--53
Sequence 53, Application US/10052586
Patent No. US20020127584A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenli
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1CI
CURRENT FILING DATE: 2002-01-15
PRIORITY APPLICATION NUMBER: US/10/052,586
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;; PRIOR APPLICATION NUMBER: 60/089908

Query Match 5 1%; Score 43.8; DB 12; Length 1998;
Best Local Similarity 47.0%; Pred. No. 0.0053;
Matches 212; Conservative 0; Mismatches 227; Indels 12; Gaps 2;

QY 224 ACGTGACAGCCGCTACCGAACCAGCCCTGATGTCACCGCGCGGATGTCGGGGCG 283
DB 402 ACCAGGACAGCGGCTATGCAACCGACGCCCTCTCCCGACCTCTGGACAGGCA 461
QY 284 ACTTCTCCCTGGCGCTTGTTCACGTCACCCCGACGACGAGAGAATTTCACCTGCG 343
DB 462 ACGCATCCCTGAGGCTGACGCGCGTGTGTGGCGGACGAGGCAAGCTTACCTGCTCG 521


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; APPLICANT: YANG, GUCHEN
; APPLICANT: LU, PIN
; APPLICANT: ZHOU, XIA-DI
; APPLICANT: PEACH, ROBERT
; TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
; FILE REFERENCE: 3053-4071US2
; CURRENT APPLICATION NUMBER: 60/272,107
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,811
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Artificial Sequence
; SEQUENCE INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Fusion construct
US-09-875-338-8

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Query Match 4.9%; Score 42.2; DB 10; Length 2097;

Best Local Similarity 46.8%; Pred. No. 0.016; Indels 12; Gaps 2;

Matches 211; Conservative 0; Mismatches 228; Indels 12; Gaps 2;

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QY 224 ACGTGACAGCCGCTACCGAACCGAGCCCTGATGTCACCGCGCGCATGTCGGGGCG 283
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DB 251 ACCAGGGCAGCGGCTATGCGAACCGAGCCCTCTTCCGGAGCTGTCGACAGGCGA 310
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QY 284 ACTTCTCCCTGCGCTGTTTCACAGTCACCCCGGAGAGCAGAGAGTTTCACTGCTGG 343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 ACGCATCCCTGAGGGCTGACGCGCTGCTGTGGCGGAGGAGGACCTTCACTGCTGG 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 344 TGTGAGCCATCCCTGGGATTCAGAGGATTTTGAAGCTTGTACATGTCATGTCG 403
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DB 371 TGAGCATCCGGGATTTGCGAGCGCTGCGCTCAAGCTGAGTGCGCCCTA----- 425
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QY 404 CAGCAAACTTCAAGCGTGCCTGCTCAGCGCCCGCCAGCCCTCCAGATGAGCTGA 463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 426 -CTGGAAGCCAGCATGAGCTGAGAGCCCAAGAGAGCTGGGGGAGGAGACGCTGA 484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 464 CCTTACGCTGATCATTAAGAGGCTACCCAGCGCCCAACGCTGACTGATCAATAAGA 523
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DB 485 CCATCACTGCTCCAGCTACAGGGCTACCTGAGGCTGAGGCTGCTGAGGATGGGC 544
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Q 524 CGAGCAACAGCGCTGAGAGCGAGGCTCTGAGATGACACCGCTTGAACATGCGGG 583
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DB 545 AGGGTGTCCCTGACTGCGAACGTCAGACGTCGAGATGGCC-----ACGAGCAGG 598
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QY 584 GCTTGTATGACGTGTGACAGCTGCTGAGATGCGACAGAGCCCGCAGCATTTGGCT 643
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DB 599 GCTTGTATGATGACACATCTCGGGGTGCTGGGTGCAATGACACTACAGCT 658
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QY 644 GCTGATAGAGACGCTTCTTGCACAGAA 674
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DB 659 GCCTGTGCGCAACCCCGCTGTCAGACAGA 689
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RESULT 12
US-09-875-338-6

; Sequence 6, Application US/09875338

; Patent No. US20020095024A1

; GENERAL INFORMATION:

; APPLICANT: MIKESSELL, GLEN E.

; APPLICANT: CHANG, HAN

; APPLICANT: FINGER, JOSHUA N.

; APPLICANT: YANG, GUCHEN

; APPLICANT: LU, PIN

; APPLICANT: ZHOU, XIA-DI

; APPLICANT: PEACH, ROBERT

```

; TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
; FILE REFERENCE: 3053-4071US2
; CURRENT APPLICATION NUMBER: 60/272,107
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,811
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-338-6

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Query Match 4.9%; Score 42.2; DB 10; Length 3197;

Best Local Similarity 46.8%; Pred. No. 0.019; Indels 12; Gaps 2;

Matches 211; Conservative 0; Mismatches 228; Indels 12; Gaps 2;

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QY 224 ACGTGACAGCCGCTACCGAACCGAGCCCTGATGTCACCGCGCGCATGTCGGGGCG 283
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DB 371 ACCAGGGCAGCGGCTATGCGAACCGAGCCCTCTTCCGGAGCTGTCGACAGGCGA 430
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DB 431 ACGCATCCCTGAGGGCTGACGCGCTGCTGTGGCGGAGGAGGACCTTCACTGCTGG 490
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QY 344 TGTGAGCCATCCCTGGGATTCAGAGGATTTTGAAGCTTGTACATGTCATGTCG 403
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DB 491 TGAGCATCCGGGATTTGCGAGCGCTGCGCTCAAGCTGAGTGCGCCCTA----- 545
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QY 404 CAGCAAACTTCAAGCGTGCCTGCTCAGCGCCCGCCAGCCCTCCAGATGAGCTGA 463
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QY 584 GCTTGTATGACGTGTGACAGCTGCTGAGATGCGACAGAGCCCGCAGCATTTGGCT 643
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QY 644 GCTGATAGAGACGCTTCTTGCACAGAA 674
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 779 GCCTGTGCGCAACCCCGCTGTCAGACAGA 809
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```

RESULT 13
US-09-875-338-19

; Sequence 19, Application US/09875338

; Patent No. US20020095024A1

; GENERAL INFORMATION:

; APPLICANT: MIKESSELL, GLEN E.

; APPLICANT: CHANG, HAN

; APPLICANT: FINGER, JOSHUA N.

; APPLICANT: YANG, GUCHEN

; APPLICANT: LU, PIN

; APPLICANT: ZHOU, XIA-DI

; APPLICANT: PEACH, ROBERT

; TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR

; FILE REFERENCE: 3053-4071US2

; CURRENT APPLICATION NUMBER: 60/272,107

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/209,811

; PRIOR FILING DATE: 2000-06-06

; PRIOR APPLICATION NUMBER: 60/272,107

; PRIOR FILING DATE: 2001-02-28

;; PRIOR APPLICATION NUMBER: 60/209, 811
;; PRIOR FILING DATE: 2000-06-06
;; NUMBER OF SEQ ID NOS: 94
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 19
;; LENGTH: 3197
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-875-338-19

Query Match 4.9%; Score 42.2; DB 10; Length 3197;
Best Local Similarity 46.8%; Pred. No. 0.019;
Matches 211; Conservative 0; Mismatches 228; Indels 12; Gaps 2;

QY 224 ACCTGACAGCCCGCTACCGGACCGAGCCCTGATGTCACCGCGGCGATGCTGCGGGCG 283
DB 371 ACCAGGGACAGCCCTATGCCACCGCAGCGCCCTTCTCCCGGACCTGCGCAGAGGCA 430
QY 284 ACTTCTCCCTGGCTTTTCACGTCACCCCGCAGAGCAGAGAGTTTCACTGCTGG 343
DB 431 ACGCATCCCTGAGGCTGCAAGCGGCTGCTGTGCGGACGAGGCGACCTTCACTGCTGG 490
QY 344 TGTGAGCCCAATCCCTGGGATTCAGAGAGTTTGAAGCTTGAAGTTACATGATG 403
DB 491 TAGGCATCCGGGATTTCCGAGCGCTGCGCTGACCTGCAAGTGCGCGCTCCCTA----- 545
QY 404 CAGCAACTTCAAGCGCTGCGCTGTCAGCGCCCGCCACAGCCCTTCCAGAGATGAGCTCA 463
DB 546 -CTCGAAGCCCGACATGACCTTGAGCCCAACAGAGACCTGCGCGCCAGGAGACAGTGA 604
QY 464 CCTTCACGTATACATCATTAACGCGCTACCCCGCAGCCAAAGTATGATGATCAATAGA 533
DB 605 CCATCAGCGTCTCCAGCTACCAAGGCGCTACCTGAGGCTGAGGTCTGTGCAAGATGGCG 664
QY 524 CGGACAACAGCCGCTGGAGCCAGGCTCTGCAAGATGACACCGCTCTTGAACATGCGG 583
DB 665 AGGGTGTGCCCTGACTGGACGTAACGTAACACGTCGCAAGATGGCC-----AACGACAGG 718
QY 584 GCTTGTATGACGTGTGACGCTGCTGAGATGCAAGGAGCCCGCAGCGTGAATGGCT 643
DB 719 GCTTGTATGATGTCACAGCATCTCGGGTGTGCTGGGTGAATGCACTACAGCT 778
QY 644 GCTGCAATAGAGACGCTTCTTGCACAGAA 674
DB 779 GCCTGTGCGCAACCCGCTGTCGACAGAGA 809

RESULT 14

US-09-875-338-10
Sequence 10, Application US/0987538
Patent No. US20020095024A1

;; GENERAL INFORMATION:
;; APPLICANT: MIKESELL, GLEN E.
;; APPLICANT: CHANG, HAN
;; APPLICANT: FINGER, JOSHUA N.
;; APPLICANT: YANG, GUCHEN
;; APPLICANT: LU, PIN
;; APPLICANT: ZHOU, XIA-DI
;; APPLICANT: PEACH, ROBERT
;; TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
;; TITLE OF INVENTION: IMMUNOMODULATION
;; FILE REFERENCE: 3053-4071052
;; CURRENT APPLICATION NUMBER: US/09/875,338
;; CURRENT FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: 60/272,107
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: 60/209,811
;; PRIOR FILING DATE: 2000-06-06
;; NUMBER OF SEQ ID NOS: 94
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 10
;; LENGTH: 951
;; TYPE: DNA

;; ORGANISM: Homo sapiens
US-09-875-338-10

Query Match 4.7%; Score 40.2; DB 10; Length 951;
Best Local Similarity 46.6%; Pred. No. 0.042;
Matches 212; Conservative 0; Mismatches 228; Indels 15; Gaps 2;

QY 229 GACAGCGCTACCGGAACCGAGCCCTGATGTCAACCGCGCGGATGCTGCGGGCGACTTC 288
DB 241 GAAGGCCGGAGCAGGAGCGCTATGCCACCGCAGCGCCCTTCCCGGACCTGCTG 300
QY 289 TCCCTGCGCTTGTTCACGTCACCCCGCAGAGCAGAGAGTTTCACTGCTGCTTG 348
DB 301 GCACAAGCAATCATCCCTGAGGCTGCAAGCGGCTGCTGTGCGGACGAGGCGACTTC 360
QY 349 AGCAATCCCTGGGATTCAGAGAGTTTGAAGCTTGAAGTTACATGCTATGCGAG-- 406
DB 361 ACCTGCTGCTGAGCATCCCGGATTTCCGAGCGCTGCGCTGAGCTGCAAGTGCGCGCT 420
QY 407 -----CAAACTTCAAGCGCTGCTGTCAGCGCCCGCCACAGCCCTTCCAGATGAG 459
DB 421 CCTACTCGAAGCCAGCATGACCTTGAGCCCAACAGAGACCTGCGCGCCAGGAGACAG 480
QY 460 CTCACCTTCAAGCTATCATTAACGCGCTACCCCGCAGCGCTGATGATCAAT 519
DB 481 GTGACCATCAGCTGCTCAAGCTACCGGGGCTACCTGAGGCTGATGCTGCGAGGAT 540
QY 520 AAGAGGAGACAGCGCTGCTGAGCGAGCTCTGCAATGACAGCGCTTCTTGAACATG 579
DB 541 GGGCAGGGTGTGCCCTGACTGGCAAGTGACACGCTGCGAGATGCC-----AACGAG 594
QY 580 CGGGCTTGTATGACGTGTGTCAGCGCTGCTGAGATGCAAGGAGCCCGCAGCGTGAACAT 639
DB 595 CAGGGCTTGTATGATGTCACAGCTGCTGCGGGTGTGCTGGGTGAATGCGACCTAC 654
QY 640 GCTGCTGATAGAGACGCTTCTTGCAGAGAA 674
DB 655 AGCTGCTGTGTCGCAACCCCGCTGTCAGACAGA 689

RESULT 15

US-09-789-561-12
Sequence 12, Application US/09789561
Patent No. US20020064818A1

;; GENERAL INFORMATION:
;; APPLICANT: NI et al.
;; TITLE OF INVENTION: 52 Human secreted proteins
;; FILE REFERENCE: PZ043P1
;; CURRENT APPLICATION NUMBER: US/09/789,561
;; CURRENT FILING DATE: 2001-02-22
;; PRIOR APPLICATION NUMBER: PCT/US00/24008
;; PRIOR FILING DATE: 2000-08-31
;; PRIOR APPLICATION NUMBER: 60/152,317
;; PRIOR FILING DATE: 1999-09-03
;; PRIOR APPLICATION NUMBER: 60/152,315
;; PRIOR FILING DATE: 1999-09-03
;; NUMBER OF SEQ ID NOS: 194
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 12
;; LENGTH: 3436
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-789-561-12

Query Match 4.7%; Score 40.2; DB 10; Length 3436;
Best Local Similarity 46.6%; Pred. No. 0.076;
Matches 212; Conservative 0; Mismatches 228; Indels 15; Gaps 2;

QY 229 GACAGCGCTACCGGAACCGAGCCCTGATGTCAACCGCGCGGATGCTGCGGGCGACTTC 288
DB 1042 GAAGGCCGGAGCAGGAGCGCTATGCCACCGCAGCGCCCTTCCCGGACCTGCTG 1101
QY 289 TCCCTGCGCTTGTTCACAGCTACCCCGCAGGAGCAGAGAGTTTCACTGCTGCTGCTG 348

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Db 1102 GCACAGGCATGCAATCCCTGAGGCTGACGCGCTGCGTGTGGCGACGAGGCGAGCTTC 1161
OY 349 AGCCAAATCCCTGGGATTTCCAGAGGTTTTCAGCTGTGAGGTTTACATGCAATGTGGCAG-- 406
Db 1162 ACCTGCTTCGTGAGCATCCGGGATTTGGCAGCGCTGCTCCATGACCTGCAAGTGTGGCGCT 1221
OY 407 -----CAACTTCAGCGGTGCGGCTGTCAGCGCCGCCACAGCCCTTCCAGATGAG 459
Db 1222 CCTACTGGAAGCCCAAGATGACCTGAGGCCCAACAAAGGACCTGCGGCGCAGGGGACAGC 1281
OY 460 CTCACCTTCAGCTGTACATCCATTAACGGCTACCCAGGCGCCAAAGTGTACTGTGATCAAT 519
Db 1282 GTGACCATCAAGTGTCTCCAGCTACCGGGCTACCTTGAAGCTGAGGTGTCTGGCAGGAT 1341
OY 520 AAGACGGAACAAGCTGCTGAGCAAGGCTCTGAGAAATGACACGCTTCTTGAACATG 579
Db 1342 GGGCAGGGGTGCGCCCTGACTGGCAAGTGAACGCTGCGAGATGCGC-----AACGAG 1395
OY 580 CGGGGCTTGTATGACGTGTGACGCTGTGAGGATGSCACGAGACCCCGACGCTGAACATT 639
Db 1396 CAGGGCTTGTGTATGTGACAGCTCTCTCGGGTGTGTGCTGTGGTGTGCAATGCACTTAC 1455
OY 640 GGCTGTGCAATAGAGAACTGCTTGTGACAGAA 674
Db 1456 AGCTGCTGTGTGCGCAACCCGCTGTGACAGAGA 1490
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Search completed: November 17, 2002, 06:45:06
Job time : 45.2984 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 17, 2002, 03:10:15 ; Search time 35.882 Seconds

(without alignments)
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Title: US-09-728-421D-11

Perfect score: 864
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Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 441362 seqs, 15338381 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43.4	5.0	3468	1 US-07-951-715A-2	Sequence 2, Appl1
2	43.4	5.0	3468	2 US-08-459-448A-2	Sequence 2, Appl1
3	43.4	5.0	3468	3 US-08-459-595A-2	Sequence 2, Appl1
4	43.4	5.0	3468	3 US-08-459-504B-2	Sequence 2, Appl1
5	43.4	5.0	3468	3 US-08-459-444-2	Sequence 2, Appl1
6	43.4	5.0	3468	3 US-09-053-549-3	Sequence 3, Appl1
7	43.4	5.0	3468	4 US-09-547-422-2	Sequence 2, Appl1
8	42.2	4.9	1602	4 US-09-651-200-11	Sequence 11, Appl1
9	42.2	4.9	2229	4 US-09-651-200-5	Sequence 5, Appl1
10	40.2	4.7	1020	4 US-09-651-200-7	Sequence 7, Appl1
11	40.2	4.7	1323	4 US-09-651-200-9	Sequence 9, Appl1
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13	40.2	4.7	2241	2 US-09-333-336A-20	Sequence 20, Appl1
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15	40.2	4.7	2241	4 US-09-402-036-20	Sequence 20, Appl1
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17	40.2	4.7	2241	4 US-09-402-036-20	Sequence 20, Appl1
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19	40.2	4.7	2241	4 US-09-402-036-20	Sequence 20, Appl1
20	40.2	4.7	2241	4 US-09-402-036-20	Sequence 20, Appl1
21	40.2	4.7	2241	4 US-09-402-036-20	Sequence 20, Appl1
22	40.2	4.7	2241	4 US-09-402-036-20	Sequence 20, Appl1
23	40.2	4.7	2241	4 US-09-402-036-20	Sequence 20, Appl1
24	40.2	4.7	2241	4 US-09-402-036-20	Sequence 20, Appl1
25	40.2	4.7	2241	4 US-09-402-036-20	Sequence 20, Appl1
26	40.2	4.7	2241	4 US-09-402-036-20	Sequence 20, Appl1
27	40.2	4.7	2241	4 US-09-402-036-20	Sequence 20, Appl1

28	40.2	4.7	2403	4 US-09-904-226-7	Sequence 7, Appl1
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30	40.2	4.7	2885	4 US-09-651-200-3	Sequence 3, Appl1
31	38.6	4.5	2370	2 US-08-838-219B-19	Sequence 19, Appl1
32	38.6	4.5	2370	3 US-09-233-336A-19	Sequence 19, Appl1
33	38.6	4.5	2370	3 US-09-233-336A-19	Sequence 19, Appl1
34	38.6	4.5	2370	4 US-09-402-036-19	Sequence 19, Appl1
35	38.6	4.5	2370	4 US-09-402-036-19	Sequence 19, Appl1
36	38.2	4.4	2435	4 US-09-484-870B-134	Sequence 134, App
37	38	4.4	1506	4 US-09-158-767-7	Sequence 7, Appl1
38	38	4.4	1506	4 US-09-158-767-8	Sequence 8, Appl1
39	38	4.4	1506	4 US-09-158-767-9	Sequence 9, Appl1
40	38	4.4	1506	4 US-09-158-767-1	Sequence 1, Appl1
41	37.6	4.4	4403765	4 US-09-103-840A-2	Sequence 2, Appl1
42	37.6	4.4	4411529	4 US-09-372-422A-21	Sequence 21, Appl1
43	37.4	4.3	1158	4 US-08-387-942C-7	Sequence 7, Appl1
44	36.6	4.2	11219	1 US-07-642-734C-1	Sequence 1, Appl1
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ALIGNMENTS

RESULT 1
US-07-951-715A-2
Sequence 2, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalin M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Lannis, Karen L.
APPLICANT: Rochstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CCG 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3468 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..3468
; OTHER INFORMATION: /product= "Full-length pure maize
; OTHER INFORMATION: optimized synthetic Bt"
; OTHER INFORMATION: /note= "Disclosed in Figure 3 as synLT.mze"
US-07-951-715A-2

Query Match
Best Local Similarity 46.3%; Score 43.4; DB 1; Length 3468;
Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

195 CCACATCCCAAGACAGCTCTTGGAAACGTGGACAGCCGCTACCGGAGACGCCCT 254
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Db 1125 CAACAACACAGAGCTGAGCGCTGAGCGGACCGAGTTGCCACGACACGACCAA 1184

QY 255 GATGTCAACGGCGCGCATGTCGGGGGAGACTTCTCCCTGGCTTCAACGTCACGCC 314
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Db 1185 CCTGCCACAGCGCGCTGTACCCAGAGCGGACCGCTGACAGCCTGGACGAGATCCCCC 1244

QY 315 CCAGAGAGACAGAAAGTTTCACTGCTGGTTGAGCCAAATCCCTGGAGTTCCAGAGGT 374
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Db 1245 CCAGAACAAACAGTGCCTCCCGCCAGGGGCTTCAGCCACCGCTGAGCCACGTGAGCAT 1304

QY 375 TTGAGCGTTAGGTTACATGTCATGTGGCAGCAAACTTCAGCGCTGCGCCGTCAGAGCG 434
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1305 GTTCGCGAGCGCTTCAGCAACAGACGAGCGTATCATCCGCCCATGTTCAAGCTG 1364

QY 435 CCCCACAGCCCTCCAGATGAGCTTCACGTTGATCATTAACGGGCTACCC 494
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1365 GATCCACCGCAGCGCGCGAGTTCAACAACATATATCCCGACGACGACGATCCCGAGATCCC 1424

QY 495 CAGGCCCAA 503
    |||||
Db 1425 CCGACCAA 1433

RESULT 2
US-08-459-448A-2
Sequence 2, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Ewola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttle, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESS: Patent & Trademark Dept., 520 White Plains
; STREET: Patent & Trademark Dept., 520 White Plains
```

```

; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIVA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3468 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..3468
; OTHER INFORMATION: /product= "Full-length pure maize
; OTHER INFORMATION: optimized synthetic Bt"
; OTHER INFORMATION: /note= "Disclosed in Figure 3 as synLT.mze"
US-08-459-448A-2

Query Match
Best Local Similarity 46.3%; Score 43.4; DB 2; Length 3468;
Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

195 CCACATCCCAAGACAGCTCTTGGAAACGTGGACAGCCGCTACCGGAGACGCCCT 254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1125 CAACAACACAGAGCTGAGCGCTGAGCGGACCGAGTTGCCACGACACGACCAA 1184

QY 255 GATGTCAACGGCGCGCATGTCGGGGGAGACTTCTCCCTGGCTTCAACGTCACGCC 314
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1185 CCTGCCACAGCGCGCTGTACCCAGAGCGGACCGCTGACAGCCTGGACGAGATCCCCC 1244

QY 315 CCAGAGAGACAGAAAGTTTCACTGCTGGTTGAGCCAAATCCCTGGAGTTCCAGAGGT 374
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1245 CCAGAACAAACAGTGCCTCCCGCCAGGGGCTTCAGCCACCGCTGAGCCACGTGAGCAT 1304

QY 375 TTGAGCGTTAGGTTACATGTCATGTGGCAGCAAACTTCAGCGCTGCGCCGTCAGAGCG 434
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Db 1305 GTTCGCGAGCGCTTCAGCAACAGACGAGCGTATCATCCGCCCATGTTCAAGCTG 1364

QY 435 CCCCACAGCCCTCCAGATGAGCTTCACGTTGATCATTAACGGGCTACCC 494
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1365 GATCCACCGCAGCGCGCGAGTTCAACAACATATATCCCGACGACGACGATCCCGAGATCCC 1424

QY 495 CAGGCCCAA 503
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Db 1425 CCGACCAA 1433
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US-08-459,595A-2
: Sequence 2, Application US/08459595A
: Patent No. 6018104
: GENERAL INFORMATION:
: APPLICANT: Kozielec, Michael G.
: APPLICANT: Desai, Nalin M.
: APPLICANT: Lewis, Kelly S.
: APPLICANT: Kramer, Vance C.
: APPLICANT: Warren, Gregory W.
: APPLICANT: Evola, Stephen V.
: APPLICANT: Crossland, Lyle D.
: APPLICANT: Wright, Martha S.
: APPLICANT: Merlino, Ellis J.
: APPLICANT: Launis, Karen L.
: APPLICANT: Rothenstein, Steven J.
: APPLICANT: Bowman, Cindy G.
: APPLICANT: Dawson, John L.
: APPLICANT: Dunder, Erik M.
: APPLICANT: Pace, Gary M.
: APPLICANT: Suttie, Janet L.
: TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
: TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6018104artis Corporation
: STREET: Patent & Trademark Dept., 520 White Plains
: STREET: Rd., POB 2005
: CITY: Tarrytown
: STATE: New York
: COUNTRY: USA
: ZIP: 10591-9005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459,595A
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/951,715
: FILING DATE: 25-SEP-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/772,027
: FILING DATE: 04-OCT-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Pace, Gary M.
: REGISTRATION NUMBER: 40403
: REFERENCE/DOCKET NUMBER: CGC 1577/CIF/DIV3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919)541-8582
: TELEFAX: (919)541-8669
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3468 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: other nucleic acid
: DESCRIPTION: /desc = "Synthetic DNA"
: HYPOTHETICAL: NO
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..3468
: OTHER INFORMATION: /product= "Full-length pure maize
: OTHER INFORMATION: optimized synthetic Bt"
: OTHER INFORMATION: /note= "Disclosed in Figure 3 as syn11.mze"
US-08-459,595A-2
Query Match 5.0%; Score 43.4; DB 3; Length 3468;
Best Local Similarity 46.3%; Pred. No. 0.035;

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	Matches	143	Conservative	0	Mismatches	166	Indels	0	Gaps	0
OY	195	CCACATCCCAAGAACACTCTCTTGGAAAACGTGACACCCTCAGCCGACCGACCT	254							
Dd	1125	CACACACAGCAGCTGCCTGTCAGCACGACCGACCGAATTCCGCTAGGCCACGAGCAA	1184							
OY	255	GATGTCACCGCGCGCATAGCTCGGGGCGACTTCTCCCTGCTTTCAACGTCACGCC	314							
Dd	1185	CCTGCCACGCGCGCTGTATCCGACAGAGGGGACCCCTGGACAGATCCCCCCC	1244							
OY	315	CCAGACAGCAGCAGAAGTTTCACTGCTTGAGCCAACTCCCTGGATTCCAGAGAGT	374							
Dd	1245	CCAGAACAAACAACGTCGCCCGCCCGCAGGGCTTCAGACCCTGAGCCACGTAGCAT	1304							
OY	375	TTTGAGCCTTGAGGTATCACTGTCATGTGGACGAACCTTCAAGCGCGCTGACGCC	434							
Dd	1305	GTTCGGCAGCGGCTTCACACACAGCAGCGGTAGCATCATCCGCCCCCATTTGAGCTG	1364							
OY	435	CCCCCAGAGCCCTCCAGATGAGCTCACTTCAGTGTATCATTAACGGCTACCC	494							
Dd	1365	GATCCACCGCAGCGCGGATTCAACACATCATCCCCCAGACCGCAGATCACCATGCC	1424							
OY	495	CAGGCCCAA	503							
Dd	1425	CCTGACCAA	1433							
RESULT 4										
US-08-459-504B-2										
Sequence 2, Application US/08459504B										
Patent No. 6075185										
GENERAL INFORMATION:										
APPLICANT: Kozziel, Michael G.										
APPLICANT: Desai, Nainil M.										
APPLICANT: Lewis, Kelly S.										
APPLICANT: Kramer, Vance C.										
APPLICANT: Warren, Gregory W.										
APPLICANT: Evola, Stephen V.										
APPLICANT: Crossland, Lyle D.										
APPLICANT: Wright, Martha S.										
APPLICANT: Merlin, Ellis J.										
APPLICANT: Launis, Karen L.										
APPLICANT: Rothstein, Steven J.										
APPLICANT: Bowman, Cindy G.										
APPLICANT: Dawson, John L.										
APPLICANT: Dunder, Erik M.										
APPLICANT: Pace, Gary M.										
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED										
NUMBER OF SEQUENCES: 94										
CORRESPONDENCE ADDRESS:										
ADDRESSEE: No. 6073185artls Corporation										
STREET: 3054 Cornwalis Road										
CITY: Research Triangle Park										
STATE: NC										
COUNTRY: USA										
ZIP: 27709										
COMPUTER READABLE FORM:										
MEDIUM TYPE: Floppy disk										
COMPUTER: IBM PC compatible										
OPERATING SYSTEM: PC-DOS/MS-DOS										
SOFTWARE: Patentin Release #1.0, Version #1.30										
CURRENT APPLICATION DATA:										
APPLICATION NUMBER: US/08/459,504B										
FILING DATE:										
CLASSIFICATION:										
PRIOR APPLICATION DATA:										
APPLICATION NUMBER: US 08/459,595										
FILING DATE: 02-JUN-1995										
APPLICATION NUMBER: US 07/951,715										
FILING DATE: 25-SEP-1992										
PRIOR APPLICATION DATA:										

QY 524 CGAACAACAGCTGCTGACAGGCTCTGCAGATGACACCGTCTTTTTCAGATGCGGG 583
DB 604 AGGGTGTGCCCCCTGACGTGACGACGTGACACGTGCGCAGATGCCC-----AACGAGAGG 657
QY 584 GCTTGTATGACGTGTGTCAGGCTGTGAGATCGCAGGAGCCCGGAGCTGTGACATTTGGCT 643
DB 658 GCTTGTGTGATGACAGCATCTCGGGGTGGTGGTGTGCAAAATGGCAGCTTACAGCT 717
QY 644 GCTGCAATAGAAACGCTCTTCTGACAGAA 674
DB 718 GCCTGTGCGCAACCCCGCTGCTGACAGAGA 748

RESULT 10

US-09-651-200-7
Sequence 7, Application US/09651200
Patent No. 6429303
GENERAL INFORMATION:
APPLICANT: Green et al
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
LYMPHOCYTE ACTIVATION ANTIGEN B-7 FAMILY AND
FILE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 1020
TYPE: DNA
ORGANISM: Homo sapiens
US-09-651-200-7

Query Match 4.7%; Score 40.2; DB 4; Length 1020;
Best Local Similarity 46.6%; Pred. No. 0.17;
Matches 212; Conservative 0; Mismatches 228; Indels 15; Gaps 2;

QY 229 GATAGCCGCTACCGAAGCGAGCTGATGTACCGCGCGGCTGTGGGGGCGCACTTC 288
DB 313 GAAGGCCGGGACCGAGCGACGCTTATGCCAACCGCAGCGCCCTCTTCCGGACGTGCTG 372
QY 289 TCCTGCGCTGTGTTCAAGCTCACCCCGCAGAGAGAGCAAAATTCTACTGCTGTGTTG 348
DB 373 GCACAAGCGCAATGCATCCCTGAGGCTGACGCGGTGTGCGGAGCAGAGGCGACCTTC 432
QY 349 AGCAATCCCTGGGATTCACAGAGGTTTGAAGGTTTACACTGATGTGCGAG-- 406
DB 433 ACCTGCTGTGAGCATCCGGGATTTCCGAGCGGTGCGCTGAGCTGAGGTGGCGGCT 492
QY 407 -----CAACTTCAGCGTCCCGGCTGTCAGCGCCCGCCCAAGCCCTCCAGATGAG 459
DB 493 CCTTACTGCAAGCCCGACATGACCTGTGAGCCCAACAGAGCCTGTGGCGCAGGAGCAG 552
QY 460 CTCACCTTACGTGTATCATTCATTAAGGCTTACCCGAGGCCCAAGCTGTACTGATCAAT 519
DB 553 GTGACCATCATCGCTGCCAGCTTACCGGGGCTTACCTGAGGCTGAGGTGCTTGTGGCAGGAT 612
QY 520 AAGAGGACAACAGCTGCTGAGCAGGCTGTGCAAAATGACACCGCTTCTTGAACATG 579
DB 613 GGGCAGGCTGTGCGCTGACTGCAACGTGACACGTGCGACATGAGCC-----AAGCAG 666
QY 580 CGGGGCTGTATGAGTGTGTCAGCGCTGAGATGCAAGCAGACCCCGCAGCTGAACATT 639
DB 667 CAGGGCTTTGTGTGATGTGACAGCGCTGCGGGGTGCTGCTGGTGTGGAATGGCAGCTTAC 726
QY 640 GGCTGCTGCATAGAGAACGTGCTTCTGACAGAGAA 674

DB 727 ACCTGCTGTGTCGCAACCCCGCTGCTGACAGAGA 761

RESULT 11

US-09-651-200-9
Sequence 9, Application US/09651200
Patent No. 6429303
GENERAL INFORMATION:
APPLICANT: Green et al
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
LYMPHOCYTE ACTIVATION ANTIGEN B-7 FAMILY AND
FILE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 1323
TYPE: DNA
ORGANISM: Homo sapiens
US-09-651-200-9

Query Match 4.7%; Score 40.2; DB 4; Length 1323;
Best Local Similarity 46.6%; Pred. No. 0.18;
Matches 212; Conservative 0; Mismatches 228; Indels 15; Gaps 2;

QY 229 GATAGCCGCTACCGAAGCGAGCTGATGTACCGCGCGGCTGTGGGGGCGCACTTC 288
DB 616 GAAGGCCGGGACCGAGCGACGCTTATGCCAACCGCAGCGCCCTCTTCCGGACGTGCTG 675
QY 289 TCCTGCGCTGTGTTCAAGCTCACCCCGCAGAGAGAGCAAAATTCTACTGCTGTGTTG 348
DB 676 GCACAAGCGCAATGCATCCCTGAGGCTGACGCGCTGCTGTCGCGGAGCAGAGGCGACCTTC 735
QY 349 AGCAATCCCTGGGATTCACAGAGGTTTGAAGGTTTACACTGATGTGCGAG-- 406
DB 736 ACCTGCTGTGAGCATCCGGGATTTCCGAGCGGTGCGCTGAGCTGAGGTGTTGCGAGAT 795
QY 407 -----CAACTTCAGCGTCCCGGCTGTCAGCGCCCGCCCAAGCCCTCCAGATGAG 459
DB 796 CCTTACTGCAAGCCCGACATGACCTGTGAGCCCAACAGAGCCTGTGGCGCAGGAGCAG 855
QY 460 CTCACCTTACGTGTATCATTCATTAAGGCTTACCCGAGGCCCAAGCTGTACTGATCAAT 519
DB 856 GTGACCATCATCGCTGCCAGCTTACCGGGGCTTACCTGAGGCTGAGGTGTTCTGCGAGAT 915
QY 520 AAGAGGACAACAGCTGCTGAGCAGGCTGTGCAAAATGACACCGCTTCTTGAACATG 579
DB 916 GGGCAGGCTGTGCGCTGACTGCAACGTGACACGTGCGACATGAGCC-----AAGCAG 969
QY 580 CGGGGCTGTATGAGTGTGTCAGCGCTGAGATGCAAGCAGACCCCGCAGCTGAACATT 639
DB 970 CAGGGCTTTGTGTGATGTGACAGCGCTGCGGGGTGCTGCTGGTGTGGAATGGCAGCTTAC 1029
QY 640 GGCTGCTGCATAGAGAACGTGCTTCTGACAGAGAA 674
DB 1030 ACCTGCTGTGTCGCAACCCCGCTGCTGACAGAGA 1064

RESULT 12

US-08-838-219B-20
Sequence 20, Application US/08838219B
Patent No. 5877012
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Kozlief, Michael G

APPLICANT: Mullins, Martha A
 APPLICANT: Nye, Gordon J
 APPLICANT: Carr, Brian
 APPLICANT: Desai, Nalini M
 APPLICANT: Kostichka, N. Kristy
 APPLICANT: Duck, Nicholas B
 APPLICANT: Estuch, Juan J
 TITLE OF INVENTION: A No. 5877012el Class of Proteins for the
 TITLE OF INVENTION: Control of Plant Pests
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: NY
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.308
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,219B
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/463,483
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/314,594
 FILING DATE: 09-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/218,018
 FILING DATE: 23-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/037,057
 FILING DATE: 25-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pace, Gary M.
 REGISTRATION NUMBER: 40,403
 REFERENCE/DOCKET NUMBER: CGC 1925
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8582
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2241 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "synthetic DNA encoding
 DESCRIPTION: VIP3A(c)"
 HYPOTHETICAL: NO
 US-08-838-219B-2

Query Match	4.7%	Score 40.2	DB 2	Length 2241
Best Local Similarity	45.6%	Pred. No. 0.21		
Matches 141	Conservative	0	Mismatches 168	Indels 0
			Gaps 0	
Oy	425 TCGTAGAGCCCCCCACAGCCCCCTCCACAGATGAGTACCTTCACAGTGCATCATCATTA	484		
Db	731 TCGGCCGACAGGCCCTTGAGAGACCGCCACGACTATATCCAGAGAGAACGTGAAGACCA	790		
Oy	485 ACGGCTAACCCACAGGCCACAGCTGTACTGATCATTAAGACGGACGAACAACGCTGTGACC	544		
Db	791 GCGGACAGGAGGTGGGCAACGTGTCAACTTCCTGATCGTGTGACGCGCCCTGCAGGCC	850		
Oy	545 AGGCTCTGCAGATGACACCGCTCTTCTTGACATCGCGGGCTTGTATGACGTGGTCAAGC	604		
Db	851 AGGCTTCTCTGACCTTGACCCCTGTCTGCAAGCTCTGTGGCTCGGCCGACATCGACTACA	910		

OY	605	TGCTGAGAAATCGCAGCGGACCCCGCGTAAACTTTGGCTGCTGCATTAAGACAGTGGCTTC	664
Db	911	CCAGCATCATGAAGCAGGCACTTGAACAAAGAGAGAGAGTTCGCGCTGGAACAATCTGC	970
OY	665	TGCAGCAGAACTCTGATCTGCGGAGGCACAGCAGGAATTCATCTGGAGAGAGACAAGA	724
Db	971	CGACCTTGAGCAACACTTTCAGCAACCCGAACTACGCCCAAGTGAAGGCGACCGCACAGG	1030
OY	725	TCACAGAGA	733
Db	1031	ACGCCAAGA	1039

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1 RESULT 13
2 US-09-233-336A-20
3 ; Sequence 20, Application US/09233336A
4 ; Patent No. 6107279
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Warren, Gregory W
7 ; APPLICANT: Koziel, Michael G
8 ; APPLICANT: Mullins, Martha A
9 ; APPLICANT: Nye, Gordon J
10 ; APPLICANT: Carr, Brian
11 ; APPLICANT: Desai, Nalini M
12 ; APPLICANT: Kostichka, N. Kristy
13 ; APPLICANT: Duck, Nicholas B
14 ; APPLICANT: Estruch, Juan J
15 ; TITLE OF INVENTION: A No. 6107279e1 Class of Proteins for the
16 ; TITLE OF INVENTION: Control of Plant Pests
17 ; NUMBER OF SEQUENCES: 20
18 ; CORRESPONDENCE ADDRESS:
19 ; ADDRESSEE: CIBA-GEIGY Corporation
20 ; STREET: 7 Skyline Drive
21 ; CITY: Hawthorne
22 ; STATE: NY
23 ; COUNTRY: USA
24 ; ZIP: 10532
25 ; COMPUTER READABLE FORM:
26 ; MEDIUM TYPE: Floppy disk
27 ; COMPUTER: IBM PC compatible
28 ; OPERATING SYSTEM: PC-DOS/MS-DOS
29 ; SOFTWARE: PatentIn Release #1.0, Version #1.30B
30 ; CURRENT APPLICATION DATA:
31 ; APPLICATION NUMBER: US/09/233,336A
32 ; FILING DATE:
33 ; CLASSIFICATION:
34 ; PRIOR APPLICATION DATA:
35 ; APPLICATION NUMBER: 08/838,219
36 ; FILING DATE:
37 ; PRIOR APPLICATION DATA:
38 ; APPLICATION NUMBER: US 08/314,594
39 ; FILING DATE: 09-SEP-1994
40 ; PRIOR APPLICATION DATA:
41 ; APPLICATION NUMBER: US 08/218,018
42 ; FILING DATE: 23-MAR-1994
43 ; PRIOR APPLICATION DATA:
44 ; APPLICATION NUMBER: US 08/037,057
45 ; FILING DATE: 25-MAR-1993
46 ; ATTORNEY/AGENT INFORMATION:
47 ; NAME: Pace, Gary M.
48 ; REGISTRATION NUMBER: 40,403
49 ; REFERENCE/DOCKET NUMBER: CGC 1925
50 ; TELECOMMUNICATION INFORMATION:
51 ; TELEPHONE: 919-541-8582
52 ; TELEFAX: 919-541-8689
53 ; INFORMATION FOR SEQ ID NO: 20:
54 ; SEQUENCE CHARACTERISTICS:
55 ; LENGTH: 2241 base pairs
56 ; TYPE: nucleic acid
57 ; STRANDEDNESS: single
58 ; TOPOLOGY: linear
59 ; MOLECULE TYPE: other nucleic acid
60 ; DESCRIPTION: /desc = "synthetic DNA encoding

```

DESCRIPTION: VIP3A(c)⁺
HYPOTHEICAL: NO
US-09-233-336A-20

Query Match
Best Local Similarity 45.6%; Score 40.2; DB 3; Length 2241;
Matches 141; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

425 TCGTCAGCGCCGCCACAGCCCTCCAGAGTACGCTCAGCTGATCCATAA 484
DB 731 TCGGCCGACGCGCCCTGAGACCGGACGAGCTGATCACCAGAGAGAGTGAAGCA 790
QY 485 ACGGCTACCCAGGCCCAACGCTGATGATCAATTAAGACGAGACGCTGCTGACC 544
DB 791 GCGGACAGGAGTGGGACAGCTGATCAACTCTGATGCTGACCGCCCTGAGGCCC 850
QY 545 AGGCTTCGAGAAATGACACCGCTCTTGAACATGGCGGCTGTATGAGTGGTGCAGC 604
DB 851 AGGCTTCCTGACCGCTGACCGCCCTGTCGCAAGCTGCTGGGCTGGCCGACATGCACTACA 910
QY 605 TCGTGAGATCGACAGGACCCCGACGCTGAACATTTGGCTCTGCATAGAGACGCTGCTTC 664
DB 911 CCAGCATCATGAGACGACCTTGACAAAGAGAGAGAGTTCGCGGTGAACATCCTGC 970
QY 665 TGCAGCAGAACTGACTGTGGGACGACGACGAGAAATGACATCGAGAGAGACAGACA 724
DB 971 CGACCTTGACCAACCTTGACCAACCCGAACTACGCCAAGGTGAAGGCGACGACGAGG 1030
QY 725 TCACAGAGA 733
DB 1031 ACGCCAAAGA 1039

RESULT 14
US-09-233-752A-20
Sequence 20, Application US/09233752A
Patent No. 6137033
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalin M
APPLICANT: Koslichka, N. Kristy
APPLICANT: Duck, Nicholas B
TITLE OF INVENTION: A No. 6137033el Class of Proteins for the
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233/752A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,219
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1925
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2241 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA encoding
DESCRIPTION: VIP3A(c)⁺
HYPOTHEICAL: NO
US-09-233-752A-20

Query Match
Best Local Similarity 45.6%; Score 40.2; DB 3; Length 2241;
Matches 141; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

425 TCGTCAGCGCCGCCACAGCCCTCCAGAGTACGCTCAGCTGATCCATAA 484
DB 731 TCGGCCGACGCGCCCTGAGACCGGACGAGCTGATCACCAGAGAGAGTGAAGCA 790
QY 485 ACGGCTACCCAGGCCCAACGCTGATGATCAATTAAGACGAGACGCTGCTGACC 544
DB 791 GCGGACAGGAGTGGGACAGCTGATCAACTCTGATGCTGACCGCCCTGAGGCCC 850
QY 545 AGGCTTCGAGAAATGACACCGCTCTTGAACATTTGGCTCTGCATAGAGACGCTGCTTC 664
DB 851 AGGCTTCCTGACCGCTGACCGCCCTGTCGCAAGCTGCTGGGCTGGCCGACATGCACTACA 910
QY 605 TCGTGAGATCGACAGGACCCCGACGCTGAACATTTGGCTCTGCATAGAGACGCTGCTTC 664
DB 911 CCAGCATCATGAGACGACCTTGACAAAGAGAGAGAGTTCGCGGTGAACATCCTGC 970
QY 665 TGCAGCAGAACTGACTGTGGGACGACGACGAGAAATGACATCGAGAGAGACAGACA 724
DB 971 CGACCTTGACCAACCTTGACCAACCCGAACTACGCCAAGGTGAAGGCGACGACGAGG 1030
QY 725 TCACAGAGA 733
DB 1031 ACGCCAAAGA 1039

RESULT 15
US-09-402-036-20
Sequence 20, Application US/09402036
Patent No. 6291156
GENERAL INFORMATION:
APPLICANT: Estruch, Juan J.
APPLICANT: Yu, Gao-Guo
APPLICANT: Warren, Gregory W.
APPLICANT: Desai, Nalin M
APPLICANT: Koziel, Michael
TITLE OF INVENTION: Plant Pest Control
FILE REFERENCE: S-21284C
CURRENT APPLICATION NUMBER: US/09/402,036
FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: PCT/EP98/01952
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 08/838,219
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/832,263

/ PRIOR FILING DATE: 1997-04-03
/ PRIOR APPLICATION NUMBER: 08/832,265
/ PRIOR FILING DATE: 1997-04-03
/ PRIOR APPLICATION NUMBER: 08/463,483
/ PRIOR FILING DATE: 1995-06-05
/ PRIOR APPLICATION NUMBER: 08/314,594
/ PRIOR FILING DATE: 1994-09-09
/ PRIOR APPLICATION NUMBER: 08/218,018
/ PRIOR FILING DATE: 1994-03-24
/ PRIOR APPLICATION NUMBER: 08/037,057
/ PRIOR FILING DATE: 1993-03-25
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 20
/ LENGTH: 2241
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
/ OTHER INFORMATION: encoding VIP3A(c)
/ 09-402-036-20

Query Match 4.7%; Score 40.2; DB 4; Length 2241;
Best Local Similarity 45.6%; Pred. No. 0.21;
Matches 141; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

QY 425 TGGTACGGCCCCCAGAGCCCTCCAGATGAGCTCACTCAGTGTACATCATTA 484
DB 731 TGGGCCGAGCGCTGAGAGACGCCAGCGAGCTGATCACCAAGAGAACGTGAGACCA 790
QY 485 ACGGCTACCCCAAGGCCCAAGTGTACTGATCAATAAGACGAGCAACAGCTGTGACC 544
DB 791 GGGGACGAGAGGTGGGCAAGTGTACTGATCGTGTGACCGGCTGTGAGGCC 850
QY 545 AGGCTGTGAGAAATGACACCGCTTCTTGAACATGCGGGGCTGTATGACGTGTCAGCG 604
DB 851 AGGCTTCTGTGACCTGACCCCTGTCGCAAGCTGCTGGGCTGTGACATGACTACA 910
QY 605 TGGTGAATGCGAGGAGCCCGAGCGTGAACATTTGGCTGTGATAGAGAACGTGCTTC 664
DB 911 CCAGCATCATGAAAGAGCACTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 970
QY 665 TGCAGCAGAACTGACTGTGCGAGCCAGACAGAAATGACATCGAGAGAGAGACAGA 724
DB 971 CGACCTGTAGCAACACTTCAAGCAACCGAACTAGCCCAAGTGAAGGCGAGCAGAGAG 1030
QY 725 TCACAGAGA 733
DB 1031 ACGCCAAGA 1039

Search completed: November 17, 2002, 05:28:47
Job time : 54.882 secs